GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 14:09:19 ; Search time 118 Seconds
(without alignments)
9.578 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 15518

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	4	2	AAW41683	Aaw41683 Peptide u
2	21	100.0	4	2	AAY31075	Aay31075 Non-cross
3	21	100.0	4	3	AAB23026	Aab23026 Human/rat
4	21	100.0	4	3	AAY67577	Aay67577 P antagon
5	21	100.0	4	4	AAB91447	Aab91447 Tachykini
6	21	100.0	4	5	ABB10091	Abb10091 Substance
7	21	100.0	4	5	AAU77846	Aau77846 Tachykini
8	18	85.7	4	1	AAP61654	Aap61654 Sequence
9	18	85.7	4	1	AAP71301	Aap71301 Peptide c
10	18	85.7	4	2	AAW41686	Aaw41686 Tetrapept
11	18	85.7	4	5	ABB10092	Abb10092 Substance
12	16	76.2	4	1	AAP61707	Aap61707 Sequence
13	16	76.2	4	1	AAP71312	Aap71312 Peptide c
14	16	76.2	4	2	AAY23485	Aay23485 V beta 6
15	16	76.2	4	3	AAB12293	Aab12293 Prodrug o
16	16	76.2	4	4	AAG62647	Aag62647 Typical t
17	16	76.2	4	5	ABB88046	Abb88046 Enzyme cl
18	15	71.4	3	3	AAY67578	Aay67578 P antagon
19	15	71.4	3	4	AAB91448	Aab91448 Tachykini
20	15	71.4	4	1	AAP60334	Aap60334 Peptide w
21	15	71.4	4	2	AAW77469	Aaw77469 Tetrapept
22	15	71.4	4	2	AAW41684	Aaw41684 Tetrapept
23	15	71.4	4	2	AAW41685	Aaw41685 Tetrapept
24	15	71.4	4	4	AAB91795	Aab91795 Amyloid b
25	15	71.4	4	4	AAB91822	Aab91822 Amyloid b
26	14	66.7	4	1	AAP61659	Aap61659 Sequence
27	14	66.7	4	1	AAP71306	Aap71306 Peptide c
28	14	66.7	4	2	AAR34486	Aar34486 FGIA. 8/1
29	14	66.7	4	2	AAR46020	Aar46020 Serine pr
30	14	66.7	4	2	AAR93149	Aar93149 Mycobacte
31	14	66.7	4	3	AAB12292	Aab12292 Prodrug o
32	14	66.7	4	4	AAB91714	Aab91714 Opioid pe
33	14	66.7	4	5	ABB88045	Abb88045 Enzyme cl
34	14	66.7	4	5	ABG32223	Abg32223 Sheep col
35	13	61.9	3	5	ABG77484	Abg77484 Targettin
36	13	61.9	4	1	AAP61658	Aap61658 Sequence
37	13	61.9	4	1	AAP71287	Aap71287 Opiate bi
38	13	61.9	4	1	AAP82691	Aap82691 Renin inh
39	13	61.9	4	2	AAR15768	Aar15768 Farnesyl-
40	13	61.9	4	2	AAR47299	Aar47299 Peptide a
41	13	61.9	4	2	AAR47301	Aar47301 Peptide a
42	13	61.9	4	2	AAR49765	Aar49765 Farnesylt
43	13	61.9	4	2	AAR77829	Aar77829 Farnesyl
44	13	61.9	4	2	AARB4314	Aar84314 Human/Bov
45	13	61.9	4	2	AAW04455	Aaw04455 Farnesyl

ALIGNMENTS

RESULT 1
AAW41683
ID AAW41683 standard; peptide; 4 AA.
XX
AC AAW41683;
XX
DT 09-JUN-1998 (first entry)
XX
DE Peptide used in ophthalmic drug to treat corneal disorders.
XX
KW Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;
KW keratitis; insulin like growth factor-I; IGF-I; eye drop.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "C-terminal amide"
XX
PN WO9749419-A1.
XX
PD 31-DEC-1997.
XX
PF 11-JUN-1997; 97WO-JP002015.
XX
PR 26-JUN-1996; 96JP-00165612.
XX
PA (SANT) SANTEN PHARM CO LTD.
XX
PI Nishida T, Nakamura M, Nakata K;
XX
DR WPI; 1998-076907/07.
XX
PT Ophthalmic drug composition containing tetra:peptide - is useful as
PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,
PT dry eye, keratitis.
XX
PS Claim 1; Page 15; 19pp; Japanese.
XX
CC The present sequence represents a tetrapeptide which is the active
CC ingredient in an ophthalmic drug composition. It is used, together with
CC insulin like growth factor-I (IGF-I), to treat corneal disorders such as
CC corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The
CC dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and
CC 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of
CC the composition is eye drops
XX
SQ Sequence 4 AA;

```
  Query Match             100.0%;  Score 21;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 2
AAY31075
ID   AAY31075 standard; peptide; 4 AA.
XX
AC   AAY31075;
XX
DT   21-OCT-1999  (first entry)
XX
DE   Non-crosslinked protein particle peptide 124.
XX
KW   Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
KW   albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /note= "C-terminal amide"
XX
PN   US5945033-A.
XX
PD   31-AUG-1999.
XX
PF   12-NOV-1996;   96US-00747137.
XX
PR   15-JAN-1991;   91US-00641720.
PR   13-OCT-1992;   92US-00959560.
PR   01-JUN-1993;   93US-00069831.
PR   14-MAR-1994;   94US-00212546.
XX
PA   (HEMO-) HEMOSPHERE INC.
XX
PI   Yen RCK;
XX
DR   WPI; 1999-508153/42.
XX
PT   Non-crosslinked protein particles for therapeutic and diagnostic use.
XX
PS   Example 22; Col 103-104; 65pp; English.
XX
CC   This invention describes a novel aqueous suspension of monodisperse
CC   particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is
CC   stable against dissolving upon dilution with an alcohol-free aqueous
CC   medium. The method involves (a) forming an aqueous solution containing
CC   albumin and hemoglobin and (b) treating the aqueous solution with an
CC   alcohol to cause the solution to become turbid. The particles are useful
CC   as agents for in vivo administration, either of their own administration
CC   or as a vehicle for other therapeutic or diagnostic agents. The method
CC   permits the formation of albumin and hemoglobin particles in the
CC   nanometer and micrometer size range, in a form closer to their natural
CC   form than the forms of the prior art. The particles therefore constitute
CC   a more closely controlled agent for in vivo administration, with greater
CC   ease of clearance from the body after their period of usefulness.
CC   AAY30952-Y31135 represent peptides used in the method of the invention
XX
SQ   Sequence 4 AA;

  Query Match             100.0%;  Score 21;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 3
AAB23026
ID   AAB23026 standard; peptide; 4 AA.
XX
AC   AAB23026;
XX
DT   16-JAN-2001  (first entry)
XX
DE   Human/rat tachykinin Substance P C-terminal tetrapeptide.
XX
KW   Substance P; tachykinin; human; rat; magnesium binding defect;
KW   sodium sensitive essential hypertension; insulin resistance;
KW   type 2 diabetes; antibody; immunoassay; quantification.
XX
OS   Homo sapiens.
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /note= "C-terminal amide"
XX
PN   WO200054053-A1.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US003707.
XX
PR   10-MAR-1999;   99US-00265690.
XX
PA   (WELL/) WELLS I C.
XX
PI   Wells IC;
XX
DR   WPI; 2000-587457/55.
XX
PT   Detecting magnesium binding defects associated with abnormal
PT   physiological states such as sodium-sensitive essential hypertension and
PT   type 2 insulin-resistant diabetes mellitus, comprises measuring a
PT   specific pentapeptide in blood.
XX
PS   Disclosure; Page 5; 21pp; English.
XX
CC   The inevntion relates to a method for detecting magnesium binding
CC   defects. The method comprises quantitating a tachykinin C-terminal
CC   pentapeptide (e.g., AAB23025) and its degradation products (e.g.,
CC   AAB23026) in blood using an antibody specific for the generalised
CC   mammalian tachykinin C-terminal pentapeptide Phe-(Phe/Val)-Gly-Leu-Met-
CC   NH2 (AAB23028). The method is useful for detecting cellular magnesium
CC   binding defects which are associated with abnormal physiological states
CC   such as sodium-sensitive essential hypertension and type 2 diabetes
CC   mellitus. The present sequence represents the C-terminal 4 amino acids of
CC   the tachykinin Substance P (AAB23027) from human and rat. This is a
CC   degradation product of the Substance P C-terminal pentapeptide (AAB23025)
CC   and may also be assayed according to the method of the invention
XX
SQ   Sequence 4 AA;

  Query Match             100.0%;  Score 21;  DB 3;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 4
AAY67577
ID   AAY67577 standard; peptide; 4 AA.
XX
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```
AC   AAY67577;
XX
DT   19-MAY-2000  (first entry)
XX
DE   P antagonist peptide #5.
XX
KW   Pharmaceutical; veterinary; gonadotropin-releasing hormone; GnRH;
KW   pore-forming agent; lecithin; stearin; P antagonist.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /note= "C-terminal amide"
XX
PN   WO200004897-A1.
XX
PD   03-FEB-2000.
XX
PF   20-JUL-1999;   99WO-AU000585.
XX
PR   20-JUL-1998;   98AU-00004730.
PR   20-JUL-1998;   98AU-00004731.
PR   13-MAY-1999;   99AU-00000324.
XX
PA   (PEPT-) PEPTECH LTD.
XX
PI   Trigg TE,  Walsh JD,  Rathjen DA;
XX
DR   WPI; 2000-182528/16.
XX
PT   Bioimplant formulation for sustained delivery of an active agent over 7
PT   days to 2 years, comprises active agent, pore-forming agent and stearin.
XX
PS   Claim 20; Page 21; 37pp; English.
XX
CC   The invention provides a pharmaceutical and/or veterinary formulation
CC   that comprises 2 -30% of active agents which include a gonadotropin-
CC   releasing hormone (GnRH) agonist, 0.5 - 20% of a pore-forming agent which
CC   is not lecithin, and the remainder stearin. The formulation is useful as
CC   a sustained release implant which can deliver the active agent for a
CC   period of 7 days to 2 years. Sequences AAY67573-578 represent P
CC   antagonist peptides used in the composition
XX
SQ   Sequence 4 AA;

  Query Match             100.0%;  Score 21;  DB 3;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 5
AAB91447
ID   AAB91447 standard; peptide; 4 AA.
XX
AC   AAB91447;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Tachykinins peptide SEQ ID NO:623.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US013576.
XX
PR   17-MAY-1999;   99US-0134406P.
PR   10-SEP-1999;   99US-0153406P.
PR   15-OCT-1999;   99US-0159783P.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity.
XX
PS   Disclosure; Page 402; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity in
CC   vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention
XX
SQ   Sequence 4 AA;

  Query Match             100.0%;  Score 21;  DB 4;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 6
ABB10091
ID   ABB10091 standard; peptide; 4 AA.
XX
AC   ABB10091;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Substance P analog used in wound healing treatment#14.
XX
KW   Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;
KW   surgical incision; burn.
XX
OS   Unidentified.
XX
PN   WO200213853-A1.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-JP006933.
XX
PR   10-AUG-2000; 2000JP-00242489.
PR   28-NOV-2000; 2000JP-00361388.
XX
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PA (SANT) SANTEN PHARM CO LTD.
PA (NISH/) NISHIDA T.
XX
PI Nishida T, Nakata K, Nakamura M;
XX
DR WPI; 2002-269153/31.
XX
PT Skin wound healing promoters or skin epidermal extension promoters
PT containing substance P analogs and insulin-like growth factor-I for
PT treating wounds like tear, abrasion, surgical incision, skin ulcers or
PT burns.
XX
PS Claim 3; Page 11; 20pp; Japanese.
XX
CC The invention relates to skin wound healing promoters, containing
CC substance P analogs or their pharmaceutically-acceptable salts, and
CC insulin-like growth factor-I as the active ingredient. The promoters are
CC for treating wounds like tears, abrasions, surgical incisions, or skin
CC ulcers and burns. The current sequence represents a substance P analog
CC for use in wound healing treatment
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 1 FGLM 4

RESULT 7
AAU77846
ID AAU77846 standard; peptide; 4 AA.
XX
AC AAU77846;
XX
DT 05-JUN-2002 (first entry)
XX
DE Tachykinin N -terminal tetrapeptide.
XX
KW Tachykinin; substance P; hypertension; hypotensive; antidiabetic;
KW gynaecological; salt-insensitive hypertension; magnesium binding;
KW insulin resistance; type 2 diabetes mellitus; pre-eclampsia; eclampsia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 4. .4
FT /note= "C terminal-amide"
XX
PN WO200211714-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US024909.
XX
PR 09-AUG-2000; 2000US-00635266.
XX
PA (MAGN-) MAGNESIUM DIAGNOSTICS INC.
XX
PI Wells IC;
XX
DR WPI; 2002-280663/32.
XX
PT New monopeptides derived from butadienes, ethylenes and propanes are
PT magnesium binding defect antagonists, useful in the treatment of e.g.
PT hypertension, insulin resistance of type 2 diabetes mellitus and
PT eclampsia.
XX
PS Disclosure; Page 2; 38pp; English.
XX
CC This invention relates to novel therapeutic compounds and methods used
CC for treating mammals with disorders such as salt-insensitive
CC hypertension. The monopeptide compounds of the invention are derived from
CC butadienes, ethylenes and propanes. The compounds of the invention are
CC used to correct a defect in magnesium binding within the plasma membranes
CC of somatic cells which results in a decrease in the intracellular
CC concentration of magnesium ions. These compounds may be used in the
CC treatment of a mammal affected with magnesium binding defect, salt-
CC sensitive (particularly hypertension), insulin resistance of type 2
CC diabetes mellitus and pre-eclampsia/eclampsia. The compounds of the
CC invention have an advantage over prior art compounds in that these
CC compounds are biologically stable. The present sequence represents the a
CC tetrapeptide from the C terminal sequence of tachykinin known as
CC substance P, this peptide is sufficient to correct the magnesium binding
CC defect responsible for causing hypertension
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 1 FGLM 4

RESULT 8
AAP61654
ID AAP61654 standard; peptide; 4 AA.
XX
AC AAP61654;
XX
DT 25-MAR-2003 (revised)
DT 03-OCT-2002 (revised)
DT 21-AUG-1991 (first entry)
XX
DE Sequence of peptide which inhibits cyclic-nucleotide independent protein
DE kinase activity and mammalian cell growth.
XX
KW Cell growth inhibitor; tumour cell growth inhibitor.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /label= Carbobenzoxy-Phe
FT Misc-difference 4
FT /label= Leu-CH2Cl
XX
PN US4582821-A.
XX
PD 15-APR-1986.
XX
PF 16-NOV-1983; 83US-00552255.
XX
PR 16-NOV-1983; 83US-00552255.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Kettner CA, Racker E;
XX
DR WPI; 1986-118872/18.
XX
PT Inhibition of tumour cell growth - using peptide and aminoacid
PT halo:methyl ketone(s).
XX
PS Claim 1; Col 4; 9pp; English.
XX
CC The cpds. of the invention inhibit protein phosphorylation. The inventors
CC claim a process for inhibiting the growth of tumour cells in a medium
CC which comprises contacting the cells with a cpd. of formula (AAP61654-
CC P61661) or a physiologically acceptable salt. (Updated on 03-OCT-2002 to

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CC   add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 4 AA;

  Query Match             85.7%;  Score 18;  DB 1;  Length 4;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              |||:
Db          1 FGLL 4


RESULT 9
AAP71301
ID   AAP71301 standard; peptide; 4 AA.
XX
AC   AAP71301;
XX
DT   25-MAR-2003  (revised)
DT   15-MAY-1991  (first entry)
XX
DE   Peptide component of cpd. for treating picornavirus infections.
XX
KW   Picornaviridae; poliovirus; rhinovirus; antiviral agent.
XX
OS   Synthetic.
XX
PN   US4636492-A.
XX
PD   13-JAN-1987.
XX
PF   29-AUG-1984;   84US-00645426.
XX
PR   29-AUG-1984;   84US-00645426.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Kettner CA, Korant BD;
XX
DR   WPI; 1987-036897/05.
XX
PT   Treating picorna-virus infection with peptide halo:methyl ketone cpds. -
PT   esp. for treating polio virus and rhino virus infections.
XX
PS   Disclosure; Page 3; 10pp; English.
XX
CC   This peptide is useful as part of a peptide/halo-methyl ketone cpd., for
CC   treating picornavirus, egpolio- or rhinovirus infections. It inhibits the
CC   processing of picornavirus capsid proteins by virus encoded proteases.
CC   See AAP71302-13. See also US4652552. (Updated on 25-MAR-2003 to correct
CC   PA field.)
XX
SQ   Sequence 4 AA;

  Query Match             85.7%;  Score 18;  DB 1;  Length 4;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              |||:
Db          1 FGLL 4


RESULT 10
AAW41686
ID   AAW41686 standard; peptide; 4 AA.
XX
AC   AAW41686;
XX
DT   09-JUN-1998  (first entry)
XX
DE   Tetrapeptide #3.
XX
KW   Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;
KW   keratitis; insulin like growth factor-I; IGF-I; eye drop.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /note= "C-terminal amide"
XX
PN   WO9749419-A1.
XX
PD   31-DEC-1997.
XX
PF   11-JUN-1997;   97WO-JP002015.
XX
PR   26-JUN-1996;   96JP-00165612.
XX
PA   (SANT ) SANTEN PHARM CO LTD.
XX
PI   Nishida T,  Nakamura M,  Nakata K;
XX
DR   WPI; 1998-076907/07.
XX
PT   Ophthalmic drug composition containing tetra:peptide - is useful as
PT   corneal disorder remedy for corneal ulcer, corneal epithelial peeling,
PT   dry eye, keratitis.
XX
PS   Disclosure; Page 11; 19pp; Japanese.
XX
CC   This sequence is shown in the specification. The invention relates to an
CC   ophthalmic drug composition which contains Phe-Gly-Leu-Met-NH2 or its
CC   medicinally acceptable salts as the active ingredient. It is used,
CC   together with insulin like growth factor-I (IGF-I), to treat corneal
CC   disorders such as corneal ulcer, corneal epithelial peeling, dry eye and
CC   keratitis. The dosage is 0.1-5000 (preferably 1-1000) mg/day of the
CC   active ingredient and 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The
CC   preferable form of the composition is eye drops
XX
SQ   Sequence 4 AA;

  Query Match             85.7%;  Score 18;  DB 2;  Length 4;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              :|||
Db          1 YGLM 4


RESULT 11
ABB10092
ID   ABB10092 standard; peptide; 4 AA.
XX
AC   ABB10092;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Substance P analog used in wound healing treatment#15.
XX
KW   Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;
KW   surgical incision; burn.
XX
OS   Unidentified.
XX
PN   WO200213853-A1.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-JP006933.
XX
PR   10-AUG-2000; 2000JP-00242489.
PR   28-NOV-2000; 2000JP-00361388.
```

```
XX
PA   (SANT ) SANTEN PHARM CO LTD.
PA   (NISH/) NISHIDA T.
XX
PI   Nishida T,  Nakata K,  Nakamura M;
XX
DR   WPI; 2002-269153/31.
XX
PT   Skin wound healing promoters or skin epidermal extension promoters
PT   containing substance P analogs and insulin-like growth factor-I for
PT   treating wounds like tear, abrasion, surgical incision, skin ulcers or
PT   burns.
XX
PS   Disclosure; Page 4; 20pp; Japanese.
XX
CC   The invention relates to skin wound healing promoters, containing
CC   substance P analogs or their pharmaceutically-acceptable salts, and
CC   insulin-like growth factor-I as the active ingredient. The promoters are
CC   for treating wounds like tears, abrasions, surgical incisions, or skin
CC   ulcers and burns. The current sequence represents a substance P analog
CC   for use in wound healing treatment
XX
SQ   Sequence 4 AA;

  Query Match             85.7%;  Score 18;  DB 5;  Length 4;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              :|||
Db          1 YGLM 4


RESULT 12
AAP61707
ID   AAP61707 standard; peptide; 4 AA.
XX
AC   AAP61707;
XX
DT   25-MAR-2003  (revised)
DT   03-OCT-2002  (revised)
DT   08-JUN-1991  (first entry)
XX
DE   Sequence located immediately adjacent to and upstream of the cleavage
DE   site within a virus-specified polypeptide precursor.
XX
KW   Viral desease; diagnosis; picornavirus.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "bonede to Boc, Z, Suc, or MeOSuc; Z=carbobenzoxy;
FT                   Boc=t-Butyloxycarbonyl; Suc=Succinyl;
FT                   MeOSuc=Methoxysuccinyl"
FT   Misc-difference 4
FT                   /note= "Bonded to a chromogenic, fluorogenic,
FT                   chemiluminescent, radioactive, antigenic, or haptenic
FT                   indicator group."
XX
PN   EP187721-A.
XX
PD   16-JUL-1986.
XX
PF   10-JAN-1986;   86EP-00300147.
XX
PR   11-JAN-1985;   85US-00690731.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Kettner CA,  Korant BD;
XX
DR   WPI; 1986-184617/29.
XX
PT   Peptide substrates for virus-specified protease(s) - with C-terminal
PT   indicator gp. linked by amide or ester linkage.
XX
PS   Example; p22; 41pp; English.
XX
CC   The cpds. of the invention are useful in diagnosis of infectious diseases
CC   caused by viruses which encode a specific protease e.g. picornaviruses.
CC   (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003
CC   to correct PA field.)
XX
SQ   Sequence 4 AA;

  Query Match             76.2%;  Score 16;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              |||
Db          1 FGL 3


RESULT 13
AAP71312
ID   AAP71312 standard; protein; 4 AA.
XX
AC   AAP71312;
XX
DT   25-MAR-2003  (revised)
DT   15-MAY-1991  (first entry)
XX
DE   Peptide component of cpd. for treating picornavirus infections.
XX
KW   Picornaviridae; poliovirus; rhinovirus; antiviral agent.
XX
OS   Synthetic.
XX
PN   US4636492-A.
XX
PD   13-JAN-1987.
XX
PF   29-AUG-1984;   84US-00645426.
XX
PR   29-AUG-1984;   84US-00645426.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Kettner CA,  Korant BD;
XX
DR   WPI; 1987-036897/05.
XX
PT   Treating picorna-virus infection with peptide halo:methyl ketone cpds. -
PT   esp. for treating polio virus and rhino virus infections.
XX
PS   Disclosure; Page 4; 10pp; English.
XX
CC   This peptide is useful as part of a peptide/halo-methyl ketone cpd., for
CC   treating picornavirus, egpolio- or rhinovirus infections. It inhibits the
CC   processing of picornavirus capsid proteins by virus encoded proteases.
CC   See AAP71301-11 and AAP71313. See also US4652552. (Updated on 25-MAR-2003
CC   to correct PA field.)
XX
SQ   Sequence 4 AA;

  Query Match             76.2%;  Score 16;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              |||
Db          1 FGL 3
```

```
RESULT 14
AAY23485
ID   AAY23485 standard; peptide; 4 AA.
XX
AC   AAY23485;
XX
DT   02-SEP-1999  (first entry)
XX
DE   V beta 6 clone found in MS patients after vaccination with TCR.
XX
KW   Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5;
KW   V beta 6.7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 6;
KW   multiple sclerosis.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9927957-A1.
XX
PD   10-JUN-1999.
XX
PF   03-DEC-1997;   97WO-US023147.
XX
PR   03-DEC-1997;   97WO-US023147.
XX
PA   (IMMU-) IMMUNE RESPONSE CORP.
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI   Brostoff SW,  Wilson DB,  Smith LR,  Gold DP,  Carlo DJ;
XX
DR   WPI; 1999-404801/34.
XX
PT   T0 cell receptor peptide-derived vaccines.
XX
PS   Example 11; Page 90; 104pp; English.
XX
CC   The specification describes vaccines which comprise immunologically
CC   effective amounts of T cell receptor (TCR) peptides. The TCRs are present
CC   on the surface of T cells. The TCRs are chosen from V beta 6.2/3, V beta
CC   6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta 13. The V beta
CC   TCR peptide-based vaccines are useful for prevention or treatment of
CC   multiple sclerosis (MS). The presence of V beta 6.7 appears to be
CC   particularly associated with multiple sclerosis and can be used to
CC   determine an individual's susceptibility to multiple sclerosis.
CC   Vaccinating, rather than passively administering heterologous antibodies,
CC   allows the host's own immune system to mobilize and suppress auto
CC   aggressive T cells. Therefore, the suppression is persistent and may
CC   involve any and all immunological mechanisms in effecting that
CC   suppression. Such a multi-faceted response is more effective than the uni
CC   -dimensional suppression achieved by passive administration of monoclonal
CC   antibodies or extant-derived regulatory T cell clones. AAY23481-Y23516
CC   represent peptides derived from TCR V beta 6 clones found in the
CC   cerebrospinal fluid (CFS) of MS patients, after vaccination with V beta 6
XX
SQ   Sequence 4 AA;

  Query Match             76.2%;  Score 16;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              |||
Db          1 FGL 3


RESULT 15
AAB12293
ID   AAB12293 standard; peptide; 4 AA.
XX
AC   AAB12293;
XX
DT   10-NOV-2000  (first entry)
XX
DE   Prodrug oligopeptide # 9.
XX
KW   Prodrug; drug; antitumour; cancer; inflammation; rheumatic disease;
KW   infection; breast; colorectal; liver; lung; prostate; ovarian; brain;
KW   pancreatic; human; chemotherapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /label= bAla
FT                   /note= "beta-Alanine"
XX
PN   WO200033888-A2.
XX
PD   15-JUN-2000.
XX
PF   10-DEC-1999;   99WO-US030393.
XX
PR   11-DEC-1998;   98US-0111793P.
PR   08-FEB-1999;   99US-0119312P.
XX
PA   (COUS ) COULTER PHARM INC.
XX
PI   Lobl TJ,  Dubois V,  Fernandez A,  Gangwar S,  Lewis E,  Nieder MH;
PI   Trouet A,  Viski P,  Yarranton GT;
XX
DR   WPI; 2000-451793/39.
XX
PT   Novel prodrug compound useful for treating cancer and inflammatory
PT   diseases comprises a therapeutic agent capable of entering a target cell,
PT   an oligopeptide, a stabilizer and optionally a linker.
XX
PS   Claim 12; Page 53; 125pp; English.
XX
CC   The present invention relates to a prodrug form of a therapeutic agent
CC   linked to an oligopeptide, which in turn is linked to a stabilising
CC   group. The present sequence is one such oligopeptide used in the present
CC   invention. The prodrug may be used in chemotherapy for the treatment of
CC   cancer such as that of breast, lung, prostate, ovary, brain or pancreas,
CC   inflammatory disorders such as rheumatic diseases and infectious diseases
XX
SQ   Sequence 4 AA;

  Query Match             76.2%;  Score 16;  DB 3;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              |||
Db          2 FGL 4


Search completed: August 25, 2004, 14:22:16
Job time : 121 secs
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Blank Sheet

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 14:18:15 ; Search time 38 Seconds
(without alignments)
10.125 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10	47.6	4	2	PT0240	Ig heavy chain CRD
2	10	47.6	4	2	A53284	T-cell receptor be
3	8	38.1	4	2	PT0633	T-cell receptor be
4	7	33.3	3	3	B23751	spinal cord peptid
5	7	33.3	4	2	E44823	synaptosomal-assoc
6	7	33.3	4	2	B53284	T-cell receptor be
7	6	28.6	3	3	GKHU	growth-modulating
8	6	28.6	3	3	A60898	bursin - chicken
9	6	28.6	3	3	A23751	spinal cord peptid
10	6	28.6	3	3	PT0636	T-cell receptor be
11	6	28.6	3	3	PT0571	T-cell receptor be
12	6	28.6	3	3	S68328	blood cell protein
13	6	28.6	4	1	ECXAA	antho-RFamide neur
14	6	28.6	4	2	A32039	tyrosine-melanocyt
15	6	28.6	4	2	ECNK	cardioexcitatory n
16	6	28.6	4	2	PL0140	carbon-monoxide de
17	6	28.6	4	2	D41654	hypothetical prote
18	6	28.6	4	2	S53508	starvation-induced
19	6	28.6	4	2	T30569	hypothetical prote
20	6	28.6	4	2	I38888	COI intron 16 prot
21	6	28.6	4	2	JQ1273	neuropeptide Antho
22	6	28.6	4	2	A35779	neuropeptide Antho
23	6	28.6	4	2	A25844	autho-RF amide neu
24	6	28.6	4	2	A60418	FMRFamide - polych
25	6	28.6	4	2	A34626	RPCH-related neuro
26	6	28.6	4	2	A32480	achatin-I - giant
27	6	28.6	4	2	S39390	myosin-light-chain
28	6	28.6	4	2	PT0271	Ig heavy chain CRD
29	6	28.6	4	2	S43959	Ig mu chain V regi
30	6	28.6	4	2	PT0711	T-cell receptor be
31	6	28.6	4	2	PT0698	T-cell receptor be
32	6	28.6	4	2	PT0677	T-cell receptor be
33	6	28.6	4	2	PT0706	T-cell receptor be
34	6	28.6	4	2	PT0675	T-cell receptor be
35	6	28.6	4	2	PT0721	T-cell receptor be
36	6	28.6	4	2	PT0566	T-cell receptor be
37	6	28.6	4	2	S47552	ubiquitin - rat
38	6	28.6	4	2	S09478	globulin IV alpha
39	5	23.8	3	3	PQ0010	angiotensin-conver
40	5	23.8	3	3	S13894	histidinol dehydro
41	5	23.8	3	3	I50412	gene p20K protein
42	5	23.8	3	3	PT0578	T-cell receptor be
43	5	23.8	3	3	I78890	tyrosine protein k
44	5	23.8	3	3	T13892	cytochrome-c oxida
45	5	23.8	4	2	S18401	thyroglobulin - do

ALIGNMENTS

RESULT 1
PT0240
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0240
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0240
A;Molecule type: DNA
A;Residues: 1-4 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 47.6%; Score 10; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GL 3
||
Db 3 GL 4

RESULT 2
A53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and j
A;Reference number: A53284; MUID:91342695; PMID:1678859
A;Accession: A53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19517.1; PID:g233917
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60739)
C;Keywords: T-cell receptor

Query Match 47.6%; Score 10; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GL 3
||
Db 1 GL 2

```
RESULT 3
PT0633
T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0633
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0633
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

  Query Match             38.1%;  Score 8;  DB 2;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GL 3
              |:
Db          3 GI 4


RESULT 4
B23751
spinal cord peptide SCP-5 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: B23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425; PMID:4015098
A;Accession: B23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <HSI>
C;Superfamily: unassigned animal peptides

  Query Match             33.3%;  Score 7;  DB 3;  Length 3;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 LM 4
              :|
Db          1 MM 2


RESULT 5
E44823
synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N;Alternate names: superprotein peptide 1
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: E44823
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A;Reference number: A44823; MUID:92044785; PMID:1941090
A;Accession: E44823
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <LOE>
A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBIP:64247)
C;Keywords: membrane trafficking

  Query Match             33.3%;  Score 7;  DB 2;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 LM 4
              :|
Db          1 IM 2


RESULT 6
B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and j
A;Reference number: A53284; MUID:91342695; PMID:1678859
A;Accession: B53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19518.1; PID:g233918
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor

  Query Match             33.3%;  Score 7;  DB 2;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FG 2
              :|
Db          2 WG 3


RESULT 7
GKHU
growth-modulating peptide - human
C;Species: Homo sapiens (man)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A01421
R;Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A;Reference number: A01421; MUID:77162369; PMID:858356
A;Accession: A01421
A;Molecule type: protein
A;Residues: 1-3 <SCH>
A;Note: this serum tripeptide is found to stimulate growth of some cell types and to inh
C;Superfamily: unassigned animal peptides

  Query Match             28.6%;  Score 6;  DB 3;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
              |
Db          1 G 1


RESULT 8
A60898
bursin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A60898
R;Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 231, 997-999, 1986
A;Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of
A;Reference number: A60898; MUID:86122916; PMID:3484838
A;Accession: A60898
A;Molecule type: protein
A;Residues: 1-3 <AUD>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; hormone
F;3/Modified site: amidated carboxyl end (Gly) #status experimental
```

```
  Query Match             28.6%;  Score 6;  DB 3;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
              |
Db          3 G 3


RESULT 9
A23751
spinal cord peptide SCP-4 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425; PMID:4015098
A;Accession: A23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <HSI>
C;Superfamily: unassigned animal peptides

  Query Match             28.6%;  Score 6;  DB 3;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
              |
Db          2 G 2


RESULT 10
PT0636
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0636
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0636
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

  Query Match             28.6%;  Score 6;  DB 3;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
              |
Db          3 G 3


RESULT 11
PT0571
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0571
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0571
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

  Query Match             28.6%;  Score 6;  DB 3;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
              |
Db          3 G 3


RESULT 12
S68328
blood cell protein A - Molgula manhattensis (fragment)
C;Species: Molgula manhattensis
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: S68328
R;Taylor, S.W.; Ross, M.M.; Waite, J.H.
Arch. Biochem. Biophys. 324, 228-240, 1995
A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from th
A;Reference number: S68325; MUID:96132650; PMID:8554314
A;Accession: S68328
A;Molecule type: protein
A;Residues: 1-3 <TAY>

  Query Match             28.6%;  Score 6;  DB 3;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 F 1
              |
Db          2 F 2


RESULT 13
ECXAA
antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
C;Accession: A26666
R;Grimmelikhuijzen, C.J.P.; Graff, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986
A;Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anem
A;Reference number: A26666; MUID:87092339; PMID:2879288
A;Accession: A26666
A;Molecule type: protein
A;Residues: 1-4 <GRI>
C;Comment: The function of this peptide is not known but it could act as a transmitter a
C;Comment: Synthetic and natural peptides had identical properties.
C;Superfamily: RFamide neuropeptide
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;4/Modified site: amidated carboxyl end (Phe) #status experimental

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
              |
Db          2 G 2


RESULT 14
A32039
tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Accession: A32039
R;Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
```

A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor
A;Reference number: A32039; MUID:89123285; PMID:2563371
A;Accession: A32039
A;Molecule type: protein
A;Residues: 1-4 <HOR>
A;Experimental source: brain
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 G 2
|
Db 4 G 4

RESULT 15
ECNK
cardioexcitatory neuropeptide FMRFamide - sunray clam
C;Species: Macrocallista nimbosa (sunray clam)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A01426
R;Price, D.A.; Greenberg, M.J.
Science 197, 670-671, 1977
A;Title: Structure of a molluscan cardioexcitatory neuropeptide.
A;Reference number: A01426; MUID:77215956; PMID:877582
A;Accession: A01426
A;Molecule type: protein
A;Residues: 1-4 <PRI>
A;Note: the active peptide was also synthesized
C;Comment: This peptide was purified from pooled extracts of cerebral, pedal, and viscer
action in molluscs; its exact physiological role is not yet established.
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; neuropeptide
F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 28.6%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
|
Db 1 F 1

Search completed: August 25, 2004, 14:25:25
Job time : 39 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 14:16:24 ; Search time 22 Seconds
(without alignments)
9.467 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	57.1	4	1	OCP1_OCTMI	P58648 octopus min
2	6	28.6	3	1	GRWM_HUMAN	P01157 homo sapien
3	6	28.6	4	1	ACH1_ACHFU	P35904 achatina fu
4	6	28.6	4	1	DCML_PSECH	P19916 pseudomonas
5	6	28.6	4	1	EOSI_HUMAN	P02731 homo sapien
6	6	28.6	4	1	FAR3_HIRME	P42562 hirudo medi
7	6	28.6	4	1	FAR4_HIRME	P42563 hirudo medi
8	6	28.6	4	1	FFKA_ANTEL	P58705 anthopleura
9	6	28.6	4	1	FLRF_HIRME	P42561 hirudo medi
10	6	28.6	4	1	FLRN_ANTEL	P58707 anthopleura
11	6	28.6	4	1	FMRF_MACNI	P01162 macrocallis
12	6	28.6	4	1	FYRI_ANTEL	P58706 anthopleura
13	6	28.6	4	1	OCP3_OCTMI	P58649 octopus min
14	5	23.8	4	1	DCMS_PSECH	P19918 pseudomonas
15	2	9.5	3	1	LUXE_VIBFI	P24272 vibrio fisc
16	1	4.8	4	1	RM01_YEAST	P36515 saccharomyc
17	0	0.0	3	1	THYL_PIG	P01151 sus scrofa
18	0	0.0	4	1	TUFT_HUMAN	P01858 homo sapien

ALIGNMENTS

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RESULT 1
OCP1_OCTMI
ID   OCP1_OCTMI      STANDARD;      PRT;      4 AA.
AC   P58648;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Cardioactive peptides Ocp-1/Ocp-2.
OS   Octopus minor (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC   Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=89766;
RN   [1]
RP   SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC   TISSUE=Brain;
RX   MEDLINE=20336815; PubMed=10876044;
RA   Iwakoshi E., Hisada M., Minakata H.;
RT   "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT   Octopus minor.";
RL   Peptides 21:623-630(2000).
CC   -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC       inotropic effects on the heart. Ocp-2 is a 1000 time less
CC       active than Ocp-1.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC   -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW   Hormone; D-amino acid.
FT   MOD_RES       2       2       D-PHENYLALANINE (IN OCP-1).
SQ   SEQUENCE   4 AA;  394 MW;  6AA879C810000000 CRC64;

  Query Match             57.1%;  Score 12;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FG 2
              ||
Db          2 FG 3


RESULT 2
GRWM_HUMAN
ID   GRWM_HUMAN      STANDARD;      PRT;      3 AA.
AC   P01157;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   Growth-modulating peptide.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77162369; PubMed=858356;
RA   Schlesinger D.H., Pickart L., Thaler M.M.;
RT   "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL   Experientia 33:324-325(1977).
CC   -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
CC       growth of some cell types and to inhibit other types in vitro.
DR   GO; GO:0001558; P:regulation of cell growth; NAS.
SQ   SEQUENCE   3 AA;  340 MW;  6331E81000000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
              |
Db          1 G 1


RESULT 3
ACH1_ACHFU
ID   ACH1_ACHFU      STANDARD;      PRT;      4 AA.
AC   P35904;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Achatin-I.
OS   Achatina fulica (Giant African snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX   NCBI_TaxID=6530;
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RN   [1]
RP   SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC   STRAIN=Ferussac; TISSUE=Ganglion;
RX   MEDLINE=89273551; PubMed=2597281;
RA   Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA   Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA   Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT   "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT   fulica Ferussac containing a D-amino acid residue.";
RL   Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN   [2]
RP   CHARACTERIZATION.
RC   STRAIN=Ferussac; TISSUE=Heart atrium;
RX   MEDLINE=91264856; PubMed=1675568;
RA   Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA   Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT   "Purification of achatin-I from the atria of the African giant snail,
RT   Achatina fulica, and its possible function.";
RL   Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=93014529; PubMed=1399265;
RA   Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA   Iwashita T., Nomoto K.;
RT   "Crystal structure and molecular conformation of achatin-I
RT   (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT   D-amino acid residue.";
RL   Int. J. Pept. Protein Res. 39:258-264(1992).
CC   -!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
CC       and produces a spike broadening of the identified heart excitatory
CC       neuron (PON); also enhances the amplitude and frequency of the
CC       heart beat. Has also an effect on several other muscles.
DR   PIR; A32480; A32480.
KW   Hormone; D-amino acid.
FT   MOD_RES       2       2       D-PHENYLALANINE.
SQ   SEQUENCE   4 AA;  408 MW;  6AADD9C810000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
               |
Db          1 G 1


RESULT 4
DCML_PSECH
ID   DCML_PSECH     STANDARD;      PRT;     4 AA.
AC   P19916;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE   dehydrogenase subunit L) (CO-DH L) (Fragment).
GN   CUTL.
OS   Pseudomonas carboxydohydrogena.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae.
OX   NCBI_TaxID=290;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90055678; PubMed=2818128;
RA   Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT   "Homology and distribution of CO dehydrogenase structural genes in
RT   carboxydotrophic bacteria.";
RL   Arch. Microbiol. 152:335-341(1989).
CC   -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC       dioxide.
CC   -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC       acceptor.
CC   -!- COFACTOR: Molybdenum (molybdopterin).
CC   -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC       SMALL.
DR   PIR; PL0140; PL0140.
KW   Oxidoreductase; Molybdenum.
FT   NON_TER       4       4
SQ   SEQUENCE   4 AA;  441 MW;  7761E876F0000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
               |
Db          2 G 2


RESULT 5
EOSI_HUMAN
ID   EOSI_HUMAN     STANDARD;      PRT;     4 AA.
AC   P02731;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   Eosinophilotactic peptides.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76078412; PubMed=1060093;
RA   Goetzl E.J., Austen K.F.;
RT   "Purification and synthesis of eosinophilotactic tetrapeptides of
RT   human lung tissue: identification as eosinophil chemotactic factor of
RT   anaphylaxis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC   -!- MISCELLANEOUS: These peptides are released from mast cells in lung
CC       (and other tissues) during hypersensitivity reactions
CC       (anaphylaxis). Their activities, preferentially affecting
CC       eosinophils, include chemotaxis, chemotactic deactivation, release
CC       of enzymes, and stimulation of the hexose monophosphate shunt.
DR   GO; GO:0006935; P:chemotaxis; IDA.
DR   GO; GO:0006955; P:immune response; IDA.
FT   VARIANT       1       1       V -> A (IN OTHER PEPTIDE).
FT                                  /FTId=VAR_005201.
SQ   SEQUENCE   4 AA;  390 MW;  6B05B862A0000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
               |
Db          2 G 2


RESULT 6
FAR3_HIRME
ID   FAR3_HIRME     STANDARD;      PRT;     4 AA.
AC   P42562;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFamide-like neuropeptide YLRF-amide.
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX   NCBI_TaxID=6421;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
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CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  598 MW;  69D4073B30000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 F 1
              |
Db          4 F 4


RESULT 7
FAR4_HIRME
ID   FAR4_HIRME     STANDARD;      PRT;     4 AA.
AC   P42563;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFamide-like neuropeptide YMRF-amide.
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX   NCBI_TaxID=6421;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  616 MW;  69D4068B30000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 F 1
              |
Db          4 F 4


RESULT 8
FFKA_ANTEL
ID   FFKA_ANTEL     STANDARD;      PRT;     4 AA.
AC   P58705;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Antho-KAamide.
OS   Anthopleura elegantissima (Sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anthopleura.
OX   NCBI_TaxID=6110;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92028852; PubMed=1681803;
RA   Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT   "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
RT   novel neuropeptide from sea anemones.";
RL   Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=93391436; PubMed=8397415;
RA   McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT   "The expansion behaviour of sea anemones may be coordinated by two
RT   inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC   -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC       groups. May be involved in the expansion phase of feeding
CC       behaviour in sea anemones.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neuron specific.
DR   PIR; JQ1273; JQ1273.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1       1       L-3-PHENYLLACTYL.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  512 MW;  6DD339C9A0000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 F 1
              |
Db          1 F 1


RESULT 9
FLRF_HIRME
ID   FLRF_HIRME     STANDARD;      PRT;     4 AA.
AC   P42561;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FLRFamide.
OS   Hirudo medicinalis (Medicinal leech), and
OS   Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX   NCBI_TaxID=6421, 27815;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=H.medicinalis;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=H.trivolvis; TISSUE=Kidney;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  582 MW;  69D40729A0000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 F 1
              |
Db          1 F 1


RESULT 10
FLRN_ANTEL
ID   FLRN_ANTEL     STANDARD;      PRT;     4 AA.
AC   P58707;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Antho-RNamide.
OS   Anthopleura elegantissima (Sea anemone).
```

```
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anthopleura.
OX   NCBI_TaxID=6110;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RX   MEDLINE=90319122; PubMed=1973541;
RA   Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA   Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT   "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
RT   anemone neuropeptide containing an unusual amino-terminal blocking
RT   group.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neuron specific.
CC   -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR   PIR; A35779; A35779.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       L-3-PHENYLLACTYL.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  549 MW;  64540729A0000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 F 1
              |
Db          1 F 1


RESULT 11
FMRF_MACNI
ID   FMRF_MACNI     STANDARD;      PRT;     4 AA.
AC   P01162;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS   Macrocallista nimbosa (Sun-ray clam),
OS   Nereis virens (Sandworm),
OS   Hirudo medicinalis (Medicinal leech), and
OS   Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC   Veneroidea; Veneridae; Macrocallista.
OX   NCBI_TaxID=6594, 6353, 6421, 27815;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
RX   MEDLINE=77215956; PubMed=877582;
RA   Price D.A., Greenberg M.J.;
RT   "Structure of a molluscan cardioexcitatory neuropeptide.";
RL   Science 197:670-671(1977).
RN   [2]
RP   SEQUENCE, AND CHARACTERIZATION.
RC   SPECIES=M.nimbosa; TISSUE=Ganglion;
RX   MEDLINE=78012038; PubMed=909875;
RA   Price D.A., Greenberg M.J.;
RT   "Purification and characterization of a cardioexcitatory neuropeptide
RT   from the central ganglia of a bivalve mollusc.";
RL   Prep. Biochem. 7:261-281(1977).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=N.virens;
RX   MEDLINE=90259866; PubMed=2342992;
RA   Krajniak K.G., Price D.A.;
RT   "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL   Peptides 11:75-77(1990).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=H.medicinalis;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [5]
RP   SEQUENCE.
RC   SPECIES=H.trivolvis; TISSUE=Kidney;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
CC       activities include augmentation, induction, and regularization of
CC       cardiac contraction.
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
DR   PIR; A01426; ECNK.
DR   PIR; A60418; A60418.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  600 MW;  69D40699A0000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 F 1
              |
Db          1 F 1


RESULT 12
FYRI_ANTEL
ID   FYRI_ANTEL     STANDARD;      PRT;     4 AA.
AC   P58706;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Antho-RIamide I [Contains: Antho-RIamide II].
OS   Anthopleura elegantissima (Sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anthopleura.
OX   NCBI_TaxID=6110;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92270459; PubMed=1821096;
RA   Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA   Grimmelikhuijzen C.J.P.;
RT   "Isolation of two novel neuropeptides from sea anemones: the unusual,
RT   biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its
RT   des-phenyllactyl fragment Tyr-Arg-Ile-NH2.";
RL   Peptides 12:1165-1173(1991).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=93391436; PubMed=8397415;
RA   McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT   "The expansion behaviour of sea anemones may be coordinated by two
RT   inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC   -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC       groups. May be involved in the expansion phase of feeding
CC       behaviour in sea anemones.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neuron specific.
KW   Neuropeptide; Amidation.
FT   CHAIN         1      4       ANTHO-RIAMIDE I.
FT   CHAIN         2      4       ANTHO-RIAMIDE II.
FT   MOD_RES       1      1       L-3-PHENYLLACTYL.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  598 MW;  60441B59A0000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 F 1
              |
Db          1 F 1


RESULT 13
OCP3_OCTMI
ID   OCP3_OCTMI     STANDARD;      PRT;     4 AA.
AC   P58649;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cardioactive peptides Ocp-3/Ocp-4.
OS   Octopus minor (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC   Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=89766;
RN   [1]
RP   SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC   TISSUE=Brain;
RX   MEDLINE=20336815; PubMed=10876044;
RA   Iwakoshi E., Hisada M., Minakata H.;
RT   "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT   Octopus minor.";
RL   Peptides 21:623-630(2000).
CC   -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC       inotropic effects on the heart. Ocp-4 is a 1000 time less
CC       active than Ocp-3.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC   -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW   Hormone; D-amino acid.
FT   MOD_RES       2       2       D-SERINE (IN OCP-4).
SQ   SEQUENCE   4 AA;  463 MW;  6AB365BB10000000 CRC64;

  Query Match             28.6%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 G 2
              |
Db          1 G 1


RESULT 14
DCMS_PSECH
ID   DCMS_PSECH     STANDARD;      PRT;     4 AA.
AC   P19918;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
DE   dehydrogenase subunit S) (CO-DH S) (Fragment).
GN   CUTS.
OS   Pseudomonas carboxydohydrogena.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae.
OX   NCBI_TaxID=290;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90055678; PubMed=2818128;
RA   Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT   "Homology and distribution of CO dehydrogenase structural genes in
RT   carboxydotrophic bacteria.";
RL   Arch. Microbiol. 152:335-341(1989).
CC   -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC       dioxide.
CC   -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC       acceptor.
CC   -!- COFACTOR: Binds 2 2Fe-2S clusters.
CC   -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC       SMALL.
DR   PIR; PL0146; PL0146.
KW   Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
FT   NON_TER       4       4
SQ   SEQUENCE   4 AA;  420 MW;  6DD33DD6F0000000 CRC64;

  Query Match             23.8%;  Score 5;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 M 4
              |
Db          1 M 1


RESULT 15
LUXE_VIBFI
ID   LUXE_VIBFI     STANDARD;      PRT;     3 AA.
AC   P24272;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE   protein synthetase) (Fragment).
GN   LUXE.
OS   Vibrio fischeri.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=668;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91072226; PubMed=2254256;
RA   Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT   "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT   site for the lux operon.";
RL   J. Bacteriol. 172:6797-6802(1990).
CC   -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC       IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC       FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC       SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC   -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC       an acyl-protein thiolester.
CC   -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M62812; -; NOT_ANNOTATED_CDS.
KW   Luminescence; Ligase.
FT   NON_TER       1       1
SQ   SEQUENCE   3 AA;  374 MW;  6AA3303000000000 CRC64;

  Query Match              9.5%;  Score 2;  DB 1;  Length 3;
  Best Local Similarity   0.0%;  Pred. No. 1.4e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 L 3
              :
Db          1 I 1


Search completed: August 25, 2004, 14:22:44
Job time : 24 secs
```

Blank Sheet

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 14:17:11 ; Search time 112 Seconds
(without alignments)
11.269 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	42.9	4	5	P83568	P83568 sepia offic
2	6	28.6	2	5	P83570	P83570 sepia offic
3	4	19.0	4	11	Q08433	Q08433 rattus sp.

ALIGNMENTS

RESULT 1
P83568
ID P83568 PRELIMINARY; PRT; 4 AA.
AC P83568;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pheromone peptide ILME.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Egg;
RX PubMed=10944467;
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia
RT officinalis.";
RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
RN [2]
RP SEQUENCE.
RC TISSUE=Egg;
RX PubMed=12207899;
RA Zatylny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
RT attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
CC -!- FUNCTION: HAS MYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OOCYTE AND EGG(EC2).
CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI.
DR GO; GO:0005186; F:pheromone activity; IEA.
KW Pheromone.
SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

Query Match 42.9%; Score 9; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LM 4
||
Db 2 LM 3

RESULT 2
P83570
ID P83570 PRELIMINARY; PRT; 2 AA.
AC P83570;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide GWa.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Optic lobe;
RX PubMed=9437704;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related
RT peptide inhibiting the motility of the mature oviduct in the
RT cuttlefish, Sepia officinalis.";
RL Peptides 18:1469-1474(1997).
CC -!- FUNCTION: REGULATORY NEUROPEPTIDE WITH MYOTROPIC ACTIVITY
CC TARGETING THE DISTAL OVIDUCT. INHIBITS THE MOTILITY OF THE OVIDUCT
CC BY DECREASING TONUS, FREQUENCY AND AMPLITUDE OF CONTRACTIONS.
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD_RES 2 2 AMIDATION.
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 28.6%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 G 2

```
                    |
Db          1 G 1
```

RESULT 3
Q08433
ID   Q08433   PRELIMINARY;   PRT;   4 AA.
AC   Q08433;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Bilirubin UDP-glucuronosyltransferase (Fragment).
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Gunn;
RX   MEDLINE=91282758; PubMed=1840486;
RA   Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT   "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT   hyperbilirubinemic Gunn rat.";
RL   Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR   EMBL; S38636; AAB19259.1; -.
DR   GO; GO:0016740; F:transferase activity; IEA.
KW   Transferase.
FT   NON_TER   1   1
SQ   SEQUENCE   4 AA; 473 MW; 633732C420000000 CRC64;

  Query Match   19.0%; Score 4; DB 11; Length 4;
  Best Local Similarity   100.0%; Pred. No. 1e+06;
  Matches   1; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          3 L 3
                |
Db          3 L 3
```

Search completed: August 25, 2004, 14:24:45
Job time : 116 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 14:24:52 ; Search time 121 Seconds
(without alignments)
10.400 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 7564

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	4	14	US-10-230-133-3	Sequence 3, Appli
2	21	100.0	4	14	US-10-053-669-2	Sequence 2, Appli
3	21	100.0	4	16	US-10-695-536-3	Sequence 3, Appli
4	16	76.2	4	9	US-09-879-442A-9	Sequence 9, Appli
5	15	71.4	3	14	US-10-230-133-2	Sequence 2, Appli
6	15	71.4	3	16	US-10-695-536-2	Sequence 2, Appli
7	14	66.7	4	9	US-09-879-442A-8	Sequence 8, Appli
8	14	66.7	4	15	US-10-137-867-328	Sequence 328, App
9	13	61.9	4	9	US-09-879-442A-98	Sequence 98, Appl
10	13	61.9	4	9	US-09-879-442A-99	Sequence 99, Appl
11	13	61.9	4	9	US-09-943-123-24	Sequence 24, Appl
12	13	61.9	4	14	US-10-087-905-30	Sequence 30, Appl
13	13	61.9	4	14	US-10-087-942-30	Sequence 30, Appl
14	13	61.9	4	14	US-10-087-402-10	Sequence 10, Appl
15	13	61.9	4	14	US-10-083-894-31	Sequence 31, Appl
16	13	61.9	4	14	US-10-196-394-98	Sequence 98, Appl
17	13	61.9	4	14	US-10-202-824-11	Sequence 11, Appl
18	13	61.9	4	15	US-10-359-363A-104	Sequence 104, App
19	12	57.1	3	14	US-10-121-857-6	Sequence 6, Appli
20	12	57.1	3	14	US-10-255-679-3	Sequence 3, Appli
21	12	57.1	3	14	US-10-208-018-6	Sequence 6, Appli
22	12	57.1	3	14	US-10-104-307-3	Sequence 3, Appli
23	12	57.1	4	8	US-08-484-409-14	Sequence 14, Appl
24	12	57.1	4	8	US-08-484-409-25	Sequence 25, Appl
25	12	57.1	4	9	US-09-804-733A-24	Sequence 24, Appl
26	12	57.1	4	9	US-09-803-126-20	Sequence 20, Appl
27	12	57.1	4	10	US-09-726-470A-29	Sequence 29, Appl
28	12	57.1	4	10	US-09-563-222-1	Sequence 1, Appli
29	12	57.1	4	10	US-09-811-945-15	Sequence 15, Appl
30	12	57.1	4	12	US-10-435-751-98	Sequence 98, Appl
31	12	57.1	4	13	US-10-007-761-62	Sequence 62, Appl
32	12	57.1	4	13	US-10-044-034-1	Sequence 1, Appli
33	12	57.1	4	13	US-10-044-034-25	Sequence 25, Appl
34	12	57.1	4	13	US-10-076-421-3	Sequence 3, Appli
35	12	57.1	4	14	US-10-087-905-14	Sequence 14, Appl
36	12	57.1	4	14	US-10-087-905-17	Sequence 17, Appl
37	12	57.1	4	14	US-10-255-679-2	Sequence 2, Appli
38	12	57.1	4	14	US-10-255-679-5	Sequence 5, Appli
39	12	57.1	4	14	US-10-255-679-11	Sequence 11, Appl
40	12	57.1	4	14	US-10-255-679-12	Sequence 12, Appl
41	12	57.1	4	14	US-10-255-679-13	Sequence 13, Appl
42	12	57.1	4	14	US-10-255-679-14	Sequence 14, Appl
43	12	57.1	4	14	US-10-255-679-16	Sequence 16, Appl
44	12	57.1	4	14	US-10-255-679-36	Sequence 36, Appl
45	12	57.1	4	14	US-10-255-679-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-10-230-133-3
; Sequence 3, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; TITLE OF INVENTION: methods for treatment of abnormal physiological states
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-10-230-133-3

Query Match 100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 1 FGLM 4

RESULT 2
US-10-053-669-2
; Sequence 2, Application US/10053669
; Publication No. US20030077658A1

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; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
;  TITLE OF INVENTION:  for Disease Diagnosis
;  FILE REFERENCE: N1427-005
;  CURRENT APPLICATION NUMBER: US/10/053,669
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 09/265,690
;  PRIOR FILING DATE: 1999-03-10
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: AMIDATION
US-10-053-669-2

  Query Match             100.0%;  Score 21;  DB 14;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 3
US-10-695-536-3
; Sequence 3, Application US/10695536
; Publication No. US20040110692A1
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert  Clifton
;  TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
;  TITLE OF INVENTION:  and Methods for Treatment of Abnormal Physiological States
;  FILE REFERENCE: 800812-0008
;  CURRENT APPLICATION NUMBER: US/10/695,536
;  CURRENT FILING DATE:  2003-10-28
;  PRIOR APPLICATION NUMBER: US 10/230,133
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US 09/635,266
;  PRIOR FILING DATE: 2000-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: AMIDATION
US-10-695-536-3

  Query Match             100.0%;  Score 21;  DB 16;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 4
US-09-879-442A-9
; Sequence 9, Application US/09879442A
; Patent No. US20020142955A1
; GENERAL INFORMATION:
;  APPLICANT: CORIXA CORPORATION
;  APPLICANT:  Dubois, Vincent
;  APPLICANT:  Fernandez, Anne Marie
;  APPLICANT:  Gangwar, Sanjeev
;  APPLICANT:  Lewis, Evan
;  APPLICANT:  Lobl, Thomas J.
;  APPLICANT:  Nieder, Matthew H.
;  APPLICANT:  Pickford, Lesley B.
;  APPLICANT:  Trouet, Andre
;  APPLICANT:  Yarranton, Geoffrey T.
;  TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS
;  FILE REFERENCE: COUL-015/02US
;  CURRENT APPLICATION NUMBER: US/09/879,442A
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: 60/290,448
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: 60/211,887
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: PCT/US99/30393
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/119,312
;  PRIOR FILING DATE: 1999-02-08
;  PRIOR APPLICATION NUMBER: 60/111,793
;  PRIOR FILING DATE: 1998-12-11
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   NAME/KEY: SITE
;   LOCATION: (1)
;   OTHER INFORMATION: Beta-Alanine
US-09-879-442A-9

  Query Match             76.2%;  Score 16;  DB 9;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              |||
Db          2 FGL 4


RESULT 5
US-10-230-133-2
; Sequence 2, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
;  TITLE OF INVENTION:  methods for treatment of abnormal physiological states
;  FILE REFERENCE: 2892-106
;  CURRENT APPLICATION NUMBER: US/10/230,133
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 09/635,266
;  PRIOR FILING DATE: 2000-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: AMIDATION
US-10-230-133-2

  Query Match             71.4%;  Score 15;  DB 14;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          2 GLM 4
              |||
Db          1 GLM 3


RESULT 6
US-10-695-536-2
; Sequence 2, Application US/10695536
; Publication No. US20040110692A1
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert  Clifton
;  TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
;  TITLE OF INVENTION:  and Methods for Treatment of Abnormal Physiological States
;  FILE REFERENCE: 800812-0008
;  CURRENT APPLICATION NUMBER: US/10/695,536
;  CURRENT FILING DATE:  2003-10-28
;  PRIOR APPLICATION NUMBER: US 10/230,133
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US 09/635,266
;  PRIOR FILING DATE: 2000-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: AMIDATION
US-10-695-536-2

  Query Match             71.4%;  Score 15;  DB 16;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GLM 4
              |||
Db          1 GLM 3


RESULT 7
US-09-879-442A-8
; Sequence 8, Application US/09879442A
; Patent No. US20020142955A1
; GENERAL INFORMATION:
;  APPLICANT: CORIXA CORPORATION
;  APPLICANT:  Dubois, Vincent
;  APPLICANT:  Fernandez, Anne Marie
;  APPLICANT:  Gangwar, Sanjeev
;  APPLICANT:  Lewis, Evan
;  APPLICANT:  Lobl, Thomas J.
;  APPLICANT:  Nieder, Matthew H.
;  APPLICANT:  Pickford, Lesley B.
;  APPLICANT:  Trouet, Andre
;  APPLICANT:  Yarranton, Geoffrey T.
;  TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS
;  FILE REFERENCE: COUL-015/02US
;  CURRENT APPLICATION NUMBER: US/09/879,442A
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: 60/290,448
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: 60/211,887
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: PCT/US99/30393
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/119,312
;  PRIOR FILING DATE: 1999-02-08
;  PRIOR APPLICATION NUMBER: 60/111,793
;  PRIOR FILING DATE: 1998-12-11
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   NAME/KEY: SITE
;   LOCATION: (1)
;   OTHER INFORMATION: Beta-Alanine
US-09-879-442A-8

  Query Match             66.7%;  Score 14;  DB 9;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              ||:
Db          2 FGI 4


RESULT 8
US-10-137-867-328
; Sequence 328, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C146
;  CURRENT APPLICATION NUMBER: US/10/137,867
;  CURRENT FILING DATE:  2002-05-03
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 328
;   LENGTH: 379
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-137-867-328

  Query Match             66.7%;  Score 14;  DB 15;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              ||:
Db          2 FGM 4


RESULT 9
US-09-879-442A-98
; Sequence 98, Application US/09879442A
; Patent No. US20020142955A1
; GENERAL INFORMATION:
;  APPLICANT: CORIXA CORPORATION
;  APPLICANT:  Dubois, Vincent
;  APPLICANT:  Fernandez, Anne Marie
;  APPLICANT:  Gangwar, Sanjeev
;  APPLICANT:  Lewis, Evan
```

```
;  APPLICANT:  Lobl, Thomas J.
;  APPLICANT:  Nieder, Matthew H.
;  APPLICANT:  Pickford, Lesley B.
;  APPLICANT:  Trouet, Andre
;  APPLICANT:  Yarranton, Geoffrey T.
;  TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS
;  FILE REFERENCE: COUL-015/02US
;  CURRENT APPLICATION NUMBER: US/09/879,442A
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: 60/290,448
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: 60/211,887
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: PCT/US99/30393
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/119,312
;  PRIOR FILING DATE: 1999-02-08
;  PRIOR APPLICATION NUMBER: 60/111,793
;  PRIOR FILING DATE: 1998-12-11
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   NAME/KEY: SITE
;   LOCATION: (1)
;   OTHER INFORMATION: 2-Thienylalanine
US-09-879-442A-98

  Query Match             61.9%;  Score 13;  DB 9;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              :||
Db          2 YGL 4


RESULT 10
US-09-879-442A-99
; Sequence 99, Application US/09879442A
; Patent No. US20020142955A1
; GENERAL INFORMATION:
;  APPLICANT: CORIXA CORPORATION
;  APPLICANT:  Dubois, Vincent
;  APPLICANT:  Fernandez, Anne Marie
;  APPLICANT:  Gangwar, Sanjeev
;  APPLICANT:  Lewis, Evan
;  APPLICANT:  Lobl, Thomas J.
;  APPLICANT:  Nieder, Matthew H.
;  APPLICANT:  Pickford, Lesley B.
;  APPLICANT:  Trouet, Andre
;  APPLICANT:  Yarranton, Geoffrey T.
;  TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS
;  FILE REFERENCE: COUL-015/02US
;  CURRENT APPLICATION NUMBER: US/09/879,442A
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: 60/290,448
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: 60/211,887
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: PCT/US99/30393
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/119,312
;  PRIOR FILING DATE: 1999-02-08
;  PRIOR APPLICATION NUMBER: 60/111,793
;  PRIOR FILING DATE: 1998-12-11
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   NAME/KEY: SITE
;   LOCATION: (1)
;   OTHER INFORMATION: Beta-Alanine
US-09-879-442A-99

  Query Match             61.9%;  Score 13;  DB 9;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              :||
Db          2 YGL 4


RESULT 11
US-09-943-123-24
; Sequence 24, Application US/09943123
; Publication No. US20020182701A1
; GENERAL INFORMATION:
;  APPLICANT: CHANG, Y-H
;  APPLICANT:  VETRO, J.A.
;  APPLICANT:  MICKA, W.S.
;  TITLE OF INVENTION: Dominant Negative Variants of Methionine Aminopeptidase
;  TITLE OF INVENTION:  2 ("MetAP2") and Clinical Uses Therefor
;  FILE REFERENCE: 16153-8007
;  CURRENT APPLICATION NUMBER: US/09/943,123
;  CURRENT FILING DATE:  2001-08-30
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  synthetic
;   OTHER INFORMATION: peptide
US-09-943-123-24

  Query Match             61.9%;  Score 13;  DB 9;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GLM 4
              |:|
Db          2 GMM 4


RESULT 12
US-10-087-905-30
; Sequence 30, Application US/10087905
; Publication No. US20030022152A1
; GENERAL INFORMATION:
;  APPLICANT: Haaland, Perry D.
;  APPLICANT:  Sherman, Douglas B.
;  APPLICANT:  Stewart II, Walter W.
;  APPLICANT:  Lloyd, Sheila A.
;  APPLICANT:  Campbell, Robert L.
;  TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR
;  TITLE OF INVENTION:  FORMULATING CULTURE MEDIA
;  FILE REFERENCE: P3250
;  CURRENT APPLICATION NUMBER: US/10/087,905
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: US/09/359,260
;  PRIOR FILING DATE: 1999-07-22
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 4
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: hypothetical
;   OTHER INFORMATION: peptide
US-10-087-905-30

  Query Match             61.9%;  Score 13;  DB 14;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              ||:
Db          2 FGV 4


RESULT 13
US-10-087-942-30
; Sequence 30, Application US/10087942
; Publication No. US20030165808A1
; GENERAL INFORMATION:
;  APPLICANT: Haaland, Perry D.
;  APPLICANT:  Sherman, Douglas B.
;  APPLICANT:  Stewart II, Walter W.
;  APPLICANT:  Lloyd, Sheila A.
;  APPLICANT:  Campbell, Robert L.
;  TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR
;  TITLE OF INVENTION:  FORMULATING CULTURE MEDIA
;  FILE REFERENCE: P3250
;  CURRENT APPLICATION NUMBER: US/10/087,942
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: US/09/359,260
;  PRIOR FILING DATE: 1999-07-22
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: hypothetical
;   OTHER INFORMATION: peptide
US-10-087-942-30

  Query Match             61.9%;  Score 13;  DB 14;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              ||:
Db          2 FGV 4


RESULT 14
US-10-087-402-10
; Sequence 10, Application US/10087402
; Publication No. US20030170748A1
; GENERAL INFORMATION:
;  APPLICANT: The Iams Company
;  APPLICANT:  Davenport, Gary Mitchell
;  APPLICANT:  Matthews, Jamie Clyde
;  TITLE OF INVENTION: Compositions and Methods for Increasing Amino Acid Absorption in
;  FILE REFERENCE: 1448.009US1
;  CURRENT APPLICATION NUMBER: US/10/087,402
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 60/273,263
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: US 60/344,088
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: tetrapeptide
US-10-087-402-10

  Query Match             61.9%;  Score 13;  DB 14;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GLM 4
              |:|
Db          2 GMM 4


RESULT 15
US-10-083-894-31
; Sequence 31, Application US/10083894
; Publication No. US20030170766A1
;   GENERAL INFORMATION:
;        APPLICANT: Brown, Michael S.
;                   Goldstein, Joseph L.
;                   Reiss, Yuval
;        TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
;                            IDENTIFICATION, CHARACTERIZATION, AND INHIBITION OF
;                            FARNESYL PROTEIN TRANSFERASE
;        NUMBER OF SEQUENCES: 52
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold, White & Durkee
;             STREET: P. O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/083,894
;             FILING DATE: 27-Feb-2002
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/07/937,893
;             FILING DATE: 18-APR-1991
;             APPLICATION NUMBER: US 07/615,713
;             FILING DATE: 20-NOV-1990
;             APPLICATION NUMBER: US 07/510,706
;             FILING DATE: 18-APR-1990
;             APPLICATION NUMBER: NOT APPLICABLE
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Parker, David L.
;             REGISTRATION NUMBER: 32,165
;             REFERENCE/DOCKET NUMBER: UTSD:249/PAR
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 512-320-7200
;             TELEFAX: 512-474-7577
;   INFORMATION FOR SEQ ID NO: 31:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 4 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-083-894-31

  Query Match             61.9%;  Score 13;  DB 14;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          2 GLM 4
              |:|
Db          2 GIM 4
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Search completed: August 25, 2004, 14:35:49
Job time : 122 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 14:20:15 ; Search time 15 Seconds
(without alignments)
13.767 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 11020

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	4	1	US-08-441-591-63	Sequence 63, Appl
2	21	100.0	4	1	US-08-303-362A-63	Sequence 63, Appl
3	21	100.0	4	4	US-09-265-690C-2	Sequence 2, Appli
4	21	100.0	4	4	US-09-635-266-3	Sequence 3, Appli
5	21	100.0	4	4	US-10-230-133-3	Sequence 3, Appli
6	21	100.0	4	5	PCT-US95-05600-80	Sequence 80, Appl
7	16	76.2	4	2	US-08-747-137-124	Sequence 124, App
8	16	76.2	4	3	US-08-722-126A-20	Sequence 20, Appl
9	15	71.4	3	4	US-09-635-266-2	Sequence 2, Appli
10	15	71.4	3	4	US-10-230-133-2	Sequence 2, Appli
11	15	71.4	4	2	US-08-070-301-8	Sequence 8, Appli
12	15	71.4	4	2	US-08-433-401-4	Sequence 4, Appli
13	14	66.7	4	3	US-08-793-701-25	Sequence 25, Appl
14	14	66.7	4	4	US-09-579-264-25	Sequence 25, Appl
15	13	61.9	4	2	US-08-429-964-37	Sequence 37, Appl
16	13	61.9	4	3	US-08-812-586-60	Sequence 60, Appl
17	13	61.9	4	4	US-08-669-656A-11	Sequence 11, Appl
18	13	61.9	4	4	US-09-535-832A-56	Sequence 56, Appl
19	13	61.9	4	4	US-09-665-362A-31	Sequence 31, Appl
20	13	61.9	4	5	PCT-US93-08062-37	Sequence 37, Appl
21	12	57.1	3	1	US-08-343-943-4	Sequence 4, Appli
22	12	57.1	3	2	US-09-060-455-2	Sequence 2, Appli
23	12	57.1	3	4	US-09-150-621-3	Sequence 3, Appli
24	12	57.1	4	1	US-07-657-769B-58	Sequence 58, Appl
25	12	57.1	4	1	US-07-822-924-3	Sequence 3, Appli
26	12	57.1	4	1	US-07-822-924-5	Sequence 5, Appli
27	12	57.1	4	1	US-07-822-924-7	Sequence 7, Appli
28	12	57.1	4	1	US-08-285-777-1	Sequence 1, Appli
29	12	57.1	4	1	US-08-147-270A-1	Sequence 1, Appli
30	12	57.1	4	1	US-07-969-307A-1	Sequence 1, Appli
31	12	57.1	4	1	US-07-969-307A-2	Sequence 2, Appli
32	12	57.1	4	1	US-07-969-307A-3	Sequence 3, Appli
33	12	57.1	4	1	US-08-127-904-11	Sequence 11, Appl
34	12	57.1	4	1	US-08-431-539-4	Sequence 4, Appli
35	12	57.1	4	1	US-08-331-383-10	Sequence 10, Appl
36	12	57.1	4	1	US-08-429-732-20	Sequence 20, Appl
37	12	57.1	4	1	US-07-789-184-108	Sequence 108, App
38	12	57.1	4	1	US-08-549-008-10	Sequence 10, Appl
39	12	57.1	4	1	US-08-624-123-11	Sequence 11, Appl
40	12	57.1	4	1	US-08-077-252B-20	Sequence 20, Appl
41	12	57.1	4	1	US-08-475-263-108	Sequence 108, App
42	12	57.1	4	1	US-08-485-886-108	Sequence 108, App
43	12	57.1	4	1	US-08-281-195A-16	Sequence 16, Appl
44	12	57.1	4	1	US-08-227-108-11	Sequence 11, Appl
45	12	57.1	4	2	US-08-459-568-29	Sequence 29, Appl

ALIGNMENTS

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RESULT 1
US-08-441-591-63
; Sequence 63, Application US/08441591
; Patent No. 5637682
;  GENERAL INFORMATION:
;    APPLICANT:  NIEUWLANDT, D., GOLD, L.  AND WECKER, M.
;    TITLE OF INVENTION:  HIGH-AFFINITY
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE LIGANDS
;    TITLE OF INVENTION:  TO THE TACHYKININ
;    TITLE OF INVENTION:  SUBSTANCE P
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MG storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,591
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/303,362
;      FILING DATE:  9-SEPTEMBER-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/931,473
;      FILING DATE:  17-AUGUST-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/117,991
;      FILING DATE:  8-SEPTEMBER 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX21/C
;    TELECOMMUNICATION INFORMATION:
```

; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-441-591-63

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 1 FGLM 4

RESULT 2
US-08-303-362A-63
; Sequence 63, Application US/08303362A
; Patent No. 5648214
; GENERAL INFORMATION:
; APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,362A
; FILING DATE: 9-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-303-362A-63

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
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Db 1 FGLM 4

RESULT 3
US-09-265-690C-2
; Sequence 2, Application US/09265690C
; Patent No. 6372440
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-2

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 1 FGLM 4

RESULT 4
US-09-635-266-3
; Sequence 3, Application US/09635266
; Patent No. 6455734
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; TITLE OF INVENTION: methods for treatment of abnormal physiological states
; FILE REFERENCE: N1427-002
; CURRENT APPLICATION NUMBER: US/09/635,266
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-09-635-266-3

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||

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Db          1 FGLM 4


RESULT 5
US-10-230-133-3
; Sequence 3, Application US/10230133
; Patent No. 6664420
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
;  TITLE OF INVENTION:  methods for treatment of abnormal physiological states
;  FILE REFERENCE: 2892-106
;  CURRENT APPLICATION NUMBER: US/10/230,133
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 09/635,266
;  PRIOR FILING DATE: 2000-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: AMIDATION
US-10-230-133-3

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  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 6
PCT-US95-05600-80
; Sequence 80, Application PC/TUS9505600
;  GENERAL INFORMATION:
;    APPLICANT:  GOLD, LARRY
;    APPLICANT:  NIEUWLANDT, DAN
;    APPLICANT:  WECKER, MATTHEW
;    APPLICANT:  SCHNEIDER, DANIEL J.
;    APPLICANT:  FEIGON, JULI
;    APPLICANT:  ALLEN, PATRICK
;    APPLICANT:  SULLENGER, BRUCE A.
;    APPLICANT:  DOUDNA, JENNIFER, A.
;    TITLE OF INVENTION:  HIGH-AFFINITY LIGANDS OF
;    TITLE OF INVENTION:  INSULIIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
;    TITLE OF INVENTION:  P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
;    NUMBER OF SEQUENCES:  239
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MG
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05600
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/238,863
;      FILING DATE:  06-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/248,632
;      FILING DATE:  24-MAY-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/303,362
;      FILING DATE:  09-SEPTEMBER-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/361,795
;      FILING DATE:  21-DECEMBER-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/117,991
;      FILING DATE:  08-SEPTEMBER-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/931,473
;      FILING DATE:  17-AUGUST-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX17/PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US95-05600-80

  Query Match             100.0%;  Score 21;  DB 5;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 7
US-08-747-137-124
; Sequence 124, Application US/08747137
; Patent No. 5945033
;  GENERAL INFORMATION:
;    APPLICANT:  YEN, Richard C.K.
;    TITLE OF INVENTION:  NON-CROSSLINKED PROTEIN PARTICLES FOR
;    TITLE OF INVENTION:  THERAPEUTIC AND DIAGNOSTIC USE
;    NUMBER OF SEQUENCES:  184
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/747,137
;      FILING DATE:  12-NOV-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/212,546
;      FILING DATE:  14-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/069,831
;      FILING DATE:  01-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/959,560
;      FILING DATE:  13-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/641,720
;      FILING DATE:  15-JAN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  016197-000840US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;  INFORMATION FOR SEQ ID NO:  124:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  /product= "Met-Amide"
US-08-747-137-124

  Query Match             76.2%;  Score 16;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              |||
Db          1 FGL 3


RESULT 8
US-08-722-126A-20
; Sequence 20, Application US/08722126A
; Patent No. 6034227
;  GENERAL INFORMATION:
;    APPLICANT:  PECHT, Israel
;    APPLICANT:  GUTHMANN, Marcelo D.
;    APPLICANT:  TAL, Michael
;    TITLE OF INVENTION:  A DNA MOLECULE ENCODING A MAST CELL
;    TITLE OF INVENTION:  FUNCTION-ASSOCIATED ANTIGEN (MAFA)
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK, P.L.L.C.
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/722,126A
;      FILING DATE:  08-OCT-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04258
;      FILING DATE:  06-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 109257
;      FILING DATE:  08-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  PECHT=1A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-722-126A-20

  Query Match             76.2%;  Score 16;  DB 3;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              |||
Db          2 FGL 4


RESULT 9
US-09-635-266-2
; Sequence 2, Application US/09635266
; Patent No. 6455734
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
;  TITLE OF INVENTION:  methods for treatment of abnormal physiological states
;  FILE REFERENCE: N1427-002
;  CURRENT APPLICATION NUMBER: US/09/635,266
;  CURRENT FILING DATE:  2000-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: AMIDATION
US-09-635-266-2

  Query Match             71.4%;  Score 15;  DB 4;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GLM 4
              |||
Db          1 GLM 3


RESULT 10
US-10-230-133-2
; Sequence 2, Application US/10230133
; Patent No. 6664420
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
;  TITLE OF INVENTION:  methods for treatment of abnormal physiological states
;  FILE REFERENCE: 2892-106
;  CURRENT APPLICATION NUMBER: US/10/230,133
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 09/635,266
;  PRIOR FILING DATE: 2000-08-09
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;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: AMIDATION
US-10-230-133-2

  Query Match             71.4%;  Score 15;  DB 4;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GLM 4
              |||
Db          1 GLM 3


RESULT 11
US-08-070-301-8
; Sequence 8, Application US/08070301
; Patent No. 5871995
;  GENERAL INFORMATION:
;    APPLICANT:  IIDA, Toshio
;    APPLICANT:  KAMINUMA, Toshihiko
;    APPLICANT:  FUSE, Yuka
;    APPLICANT:  TAJIMA, Masahiro
;    APPLICANT:  YANAGI, Mitsuo
;    APPLICANT:  OKAMOTO, Hiroshi
;    APPLICANT:  KISHIMOTO, Jiro
;    APPLICANT:  IFUKU, Ohji
;    APPLICANT:  KATO, Ichiro
;    TITLE OF INVENTION:  ENZYME PARTICIPATING IN C-TERMINAL
;    TITLE OF INVENTION:  AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wegner, Cantor, Mueller & Player, P.C.
;      STREET:  1233 20th Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20036-8218
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/070,301
;      FILING DATE:  24-MAY-1991
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-209687
;      FILING DATE:  15-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-181933
;      FILING DATE:  31-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-76331
;      FILING DATE:  26-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-106412
;      FILING DATE:  24-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-205475
;      FILING DATE:  02-AUG-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  P-450-22830
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-040
;      TELEFAX:  (202) 835-0605
;      TELEX:  440706
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-070-301-8

  Query Match             71.4%;  Score 15;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GLM 4
              |||
Db          1 GLM 3


RESULT 12
US-08-433-401-4
; Sequence 4, Application US/08433401
; Patent No. 5872097
;  GENERAL INFORMATION:
;    APPLICANT:  Fh lenhag, Karin I.
;    APPLICANT:  Fryklund, Linda
;    APPLICANT:  Larsson, Bo C.
;    APPLICANT:  Nyberg, Fred J.
;    APPLICANT:  Westin-Sj dahl, Gertrud E.
;    APPLICANT:  Ludin, Ronny
;    TITLE OF INVENTION:  New Oligopeptides with Affinity to
;    TITLE OF INVENTION:  Opioid Receptors
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pollock, Vande Sande & Priddy
;      STREET:  1990 M Street, N.W., Suite 800
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20036-0088
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/433,401
;      FILING DATE:  18-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT\SE93\00986
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9203496-6
;      FILING DATE:  20-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Amernick, Burton A.
;      REGISTRATION NUMBER:  24,852
;      REFERENCE/DOCKET NUMBER:  151/00118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 331-7111
;      TELEFAX:  (202) 223-2596
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-433-401-4
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```
  Query Match             71.4%;  Score 15;  DB 2;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              :||:
Db          1 YGLL 4


RESULT 13
US-08-793-701-25
; Sequence 25, Application US/08793701
; Patent No. 6248581
;  GENERAL INFORMATION:
;    APPLICANT:  GICQUEL, Brigitte
;    APPLICANT:  LIM, Eng Mong
;    APPLICANT:  PORTNOI, Denis
;    APPLICANT:  BERTHET, Francois-Xavier
;    APPLICANT:  TIMM, Juliano
;    TITLE OF INVENTION:  MYCOBACTERIA FUNCTIONAL SCREENING AND/OR
;    TITLE OF INVENTION:  EXPRESSION VECTORS
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FINNEGAN, HENDERSON, FARRABOW, GARRETT &
;      ADDRESSEE:  DUNNER, L.L.P.
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,701
;      FILING DATE:  09-JUN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/FR9501133
;      FILING DATE:  30-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 94/10585
;      FILING DATE:  02-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDonell, Leslie A.
;      REGISTRATION NUMBER:  34,872
;      REFERENCE/DOCKET NUMBER:  02356.0075
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4132
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-793-701-25

  Query Match             66.7%;  Score 14;  DB 3;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 3e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              ||:
Db          2 FGI 4


RESULT 14
US-09-579-264-25
; Sequence 25, Application US/09579264
; Patent No. 6565855
;  GENERAL INFORMATION:
;    APPLICANT:  GICQUEL, Brigitte
;    APPLICANT:  LIM, Eng Mong
;    APPLICANT:  PORTNOI, Denis
;    APPLICANT:  BERTHET, Francois-Xavier
;    APPLICANT:  TIMM, Juliano
;    TITLE OF INVENTION:  MYCOBACTERIA FUNCTIONAL SCREENING AND/OR
;    TITLE OF INVENTION:  EXPRESSION VECTORS
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FINNEGAN, HENDERSON, FARRABOW, GARRETT &
;      ADDRESSEE:  DUNNER, L.L.P.
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/579,264
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/793,701
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 94/10585
;      FILING DATE:  02-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDonell, Leslie A.
;      REGISTRATION NUMBER:  34,872
;      REFERENCE/DOCKET NUMBER:  02356.0075
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4132
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-579-264-25

  Query Match             66.7%;  Score 14;  DB 4;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 3e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGL 3
              ||:
Db          2 FGI 4


RESULT 15
US-08-429-964-37
; Sequence 37, Application US/08429964
; Patent No. 5962243
;  GENERAL INFORMATION:
;    APPLICANT:  BROWN, MICHAEL S.
;    APPLICANT:  GOLDSTEIN, JOSEPH L.
;    APPLICANT:  REISS, YUVAL
;    APPLICANT:  JAMES, GUY L.
;    TITLE OF INVENTION:  METHODS FOR THE IDENTIFICATION OF FARNESYL
;    TITLE OF INVENTION:  TRANSFERASE INHIBITORS
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
```

```
;       STATE:  TEXAS
;       COUNTRY:  UNITED STATES OF AMERICA
;       ZIP:  77210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS/ASCII
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/429,964
;       FILING DATE:  27-APR-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/021,625
;       FILING DATE:  16-FEB-1993
;       CLASSIFICATION:  435
;       APPLICATION NUMBER:  US 07/822,011
;       FILING DATE:  ABANDONED
;       CLASSIFICATION:  435
;       APPLICATION NUMBER:  PCT/US/91/02650
;       FILING DATE:  18-APR-1991
;       CLASSIFICATION:  435
;       APPLICATION NUMBER:  US 07/615,715
;       FILING DATE:  20-NOV-1990
;       CLASSIFICATION:  435
;       APPLICATION NUMBER:  US 07/510,706
;       FILING DATE:  18-APR-1990 (ABANDONED)
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PARKER, DAVID L.
;       REGISTRATION NUMBER:  32,165
;       REFERENCE/DOCKET NUMBER:  UTSD:432/PAR
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (512) 418-3000
;       TELEFAX:  (713) 789-2679
;       TELEX:  79-0924
;   INFORMATION FOR SEQ ID NO:  37:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-429-964-37

  Query Match             61.9%;  Score 13;  DB 2;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 3e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GLM 4
              |:|
Db          2 GIM 4


Search completed: August 25, 2004, 14:25:47
Job time : 16 secs
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Blank Sheet

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 13:57:37 ; Search time 39 Seconds
(without alignments)
9.866 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	11	1	SPHO	substance P - hors
2	21	100.0	11	1	A60654	substance P - guin
3	21	100.0	11	2	JN0023	substance P - chic
4	21	100.0	11	2	F60409	substance P-like p
5	21	100.0	11	2	E60409	substance P-like p
6	21	100.0	11	2	S23308	substance P - rain
7	21	100.0	11	2	S33300	probable substance
8	21	100.0	19	2	PS0332	phospholipase A2 (
9	21	100.0	56	2	A69983	hypothetical prote
10	21	100.0	63	2	JC2412	tachykinin gamma c
11	21	100.0	69	2	S04666	hypothetical prote
12	21	100.0	72	2	I62742	tachykinin A gamma
13	21	100.0	72	2	JC5455	preprotachykinin-A
14	21	100.0	72	2	T25860	hypothetical prote
15	21	100.0	78	2	AE3165	hypothetical prote
16	21	100.0	80	2	T11069	NADH2 dehydrogenas
17	21	100.0	85	2	H69191	hypothetical prote
18	21	100.0	89	2	S72598	sulfate permease T
19	21	100.0	90	2	A65037	hypothetical 9.9 k
20	21	100.0	90	2	C85905	hypothetical prote
21	21	100.0	90	2	E91060	hypothetical prote
22	21	100.0	97	2	S12958	tachykinin delta p
23	21	100.0	102	2	G72756	hypothetical prote
24	21	100.0	105	2	F72614	hypothetical prote
25	21	100.0	106	2	G81275	hypothetical prote
26	21	100.0	109	2	I52333	G1 phase-specific
27	21	100.0	110	2	G69609	cytochrome-c oxida
28	21	100.0	112	1	SPRTA	substance P alpha
29	21	100.0	112	2	T51238	scarecrow-like pro
30	21	100.0	115	1	SPRBG	substance P gamma
31	21	100.0	115	2	S47039	tachykinin 1 precu
32	21	100.0	116	2	H83167	hypothetical prote
33	21	100.0	116	2	C72232	hypothetical prote
34	21	100.0	117	2	A71391	NADH2 dehydrogenas
35	21	100.0	117	2	G64486	hypothetical prote
36	21	100.0	124	2	B86771	hypothetical prote
37	21	100.0	124	2	E97098	Zn-finger containi
38	21	100.0	126	2	S70624	cytochrome P450 CY
39	21	100.0	128	2	A88072	protein ZK1240.6 [
40	21	100.0	129	1	SPHUB	neurokinin 1 precu
41	21	100.0	129	2	A82227	conserved hypothet
42	21	100.0	130	1	SPRTB	substance P beta p
43	21	100.0	130	1	SPBOB	neurokinin 1 precu
44	21	100.0	130	2	S47038	tachykinin 1 precu
45	21	100.0	130	2	I52526	neurokinin 1 precu

ALIGNMENTS

RESULT 1
SPHO
substance P - horse
C;Species: Equus caballus (domestic horse)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996
C;Accession: A01558
R;Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.
A;Reference number: A01558
A;Accession: A01558
A;Molecule type: protein
A;Residues: 1-11 <STU>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 8 FGLM 11

RESULT 2
A60654
substance P - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995
C;Accession: A60654
R;Murphy, R.
Neuropeptides 14, 105-110, 1989
A;Title: Primary amino acid sequence of guinea-pig substance P.
A;Reference number: A60654; MUID:90044685; PMID:2478925
A;Accession: A60654
A;Molecule type: protein
A;Residues: 1-11 <MUR>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 8 FGLM 11

```
RESULT 3
JN0023
substance P - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C;Accession: JN0023
R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A;Reference number: JN0023; MUID:88204263; PMID:2452461
A;Accession: JN0023
A;Molecule type: protein
A;Residues: 1-11 <CON>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

  Query Match             100.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          8 FGLM 11


RESULT 4
F60409
substance P-like peptide II - frog (Pseudophryne guentheri)
C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C;Accession: F60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austra
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: F60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

  Query Match             100.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          8 FGLM 11


RESULT 5
E60409
substance P-like peptide I - frog (Pseudophryne guentheri)
C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C;Accession: E60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austra
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: E60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

  Query Match             100.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          8 FGLM 11


RESULT 6
S23308
substance P - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C;Accession: S23308
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod
A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23308
A;Molecule type: protein
A;Residues: 1-11 <JEN>
A;Experimental source: brain
C;Function:
A;Description: may play a physiological role in the regulation of cardiovascular and gas
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

  Query Match             100.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          8 FGLM 11


RESULT 7
S33300
probable substance P - smaller spotted catshark
C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
C;Accession: S33300
R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.
Eur. J. Biochem. 214, 469-474, 1993
A;Title: Primary structures and biological activities of substance-P-related peptides fr
A;Reference number: S33300; MUID:93292508; PMID:7685693
A;Accession: S33300
A;Molecule type: protein
A;Residues: 1-11 <WAU>
A;Experimental source: brain
C;Function:
A;Description: may play a physiological role in the regulation of cardiovascular and ga
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

  Query Match             100.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          8 FGLM 11


RESULT 8
PS0332
phospholipase A2 (EC 3.1.1.4), sperm - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Mar-2000
C;Accession: PS0332
R;Langlais, J.; Chafouleas, J.G.; Ingraham, R.; Vigneault, N.; Roberts, K.D.
```

Biochem. Biophys. Res. Commun. 182, 208-214, 1992
A;Title: The phospholipase A2 of human spermatozoa; purification and partial sequence.
A;Reference number: PS0332; MUID:92118015; PMID:1731781
A;Accession: PS0332
A;Molecule type: protein
A;Residues: 1-19 <LAN>
C;Keywords: carboxylic ester hydrolase

Query Match 100.0%; Score 21; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 5 FGLM 8

RESULT 9
A69983
hypothetical protein yrzK - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: A69983
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: A69983
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-56 <KUN>
A;Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14716.1; PID:e1184005;
A;Experimental source: strain 168
C;Genetics:
A;Gene: yrzK

Query Match 100.0%; Score 21; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 39 FGLM 42

RESULT 10
JC2412
tachykinin gamma chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: JC2412
R;Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A;Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in th
A;Reference number: JC2411; MUID:94324969; PMID:7519424
A;Accession: JC2412
A;Molecule type: mRNA
A;Residues: 1-63 <KHA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end
F;12-21/Product: substance P #status predicted <SUP>
F;21/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 100.0%; Score 21; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 18 FGLM 21

RESULT 11
S04666
hypothetical protein 1 - Rhodopseudomonas blastica (fragment)
C;Species: Rhodopseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
C;Accession: S04666
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04666
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-69 <TYB>

Query Match 100.0%; Score 21; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 18 FGLM 21

RESULT 12
I62742
tachykinin A gamma chain precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Accession: I62742; JC5453
R;Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A;Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A;Reference number: JC5450; MUID:91209287; PMID:1708336
A;Accession: I62742
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-72 <RES>
A;Cross-references: GB:M68909; NID:g200469; PIDN:AAA39970.1; PID:g554261
C;Comment: This protein contains two tachykinin peptide hormone substance-P which is inv
C;Genetics:
A;Gene: gamma-PPT-A
C;Superfamily: substance P precursor
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-33/Product: substance-P #status predicted <STP>
F;48-57/Product: neurokinin-A #status predicted <NKA>

Query Match 100.0%; Score 21; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 30 FGLM 33

RESULT 13
JC5455
preprotachykinin-A gamma precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 16-Jul-1999
C;Accession: JC5455; I45967

R;Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A;Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A;Reference number: JC5450; MUID:91209287; PMID:1708336
A;Accession: JC5455
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-72 <CHI>
A;Cross-references: GB:M68912; NID:g163593; PIDN:AAA30725.1; PID:g552336
C;Comment: This protein contains two tachykinin peptide hormone substance-P which is inv
C;Genetics:
A;Gene: PPT-A
C;Superfamily: substance P precursor
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-33/Product: substance-P #status predicted <STP>
F;48-57/Product: neurokinin-A #status predicted <NKA>

  Query Match 100.0%; Score 21; DB 2; Length 72;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 30 FGLM 33

RESULT 14
T25860
hypothetical protein T04C9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25860
R;Favello, A.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid T04C9.
A;Reference number: Z20101
A;Accession: T25860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-72 <FAV>
A;Cross-references: EMBL:U80955; PIDN:AAB38101.1; GSPDB:GN00021; CESP:T04C9.3
A;Experimental source: strain Bristol N2; clone T04C9
C;Genetics:
A;Gene: CESP:T04C9.3
A;Map position: 3

  Query Match 100.0%; Score 21; DB 2; Length 72;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 24 FGLM 27

RESULT 15
AE3165
hypothetical protein Atu5047 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AE3165
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE3165
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-78 <KUR>
A;Cross-references: GB:AE008687; PIDN:AAL45739.1; PID:g17743471; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5047
A;Genome: plasmid

  Query Match 100.0%; Score 21; DB 2; Length 78;
  Best Local Similarity 100.0%; Pred. No. 1.4e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 22 FGLM 25

Search completed: August 25, 2004, 14:07:11
Job time : 48 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 13:41:56 ; Search time 22 Seconds
(without alignments)
9.467 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	21	100.0	11	1	TKN4_PSEGU	P42989	pseudophryn
2	21	100.0	11	1	TKN5_PSEGU	P42990	pseudophryn
3	21	100.0	11	1	TKNA_CHICK	P19850	gallus gall
4	21	100.0	11	1	TKNA_HORSE	P01290	equus cabal
5	21	100.0	11	1	TKNA_ONCMY	P28499	oncorhynchu
6	21	100.0	11	1	TKNA_SCYCA	P41333	scyliorhinu
7	21	100.0	19	1	PA2S_HUMAN	P24606	homo sapien
8	21	100.0	56	1	YRZK_BACSU	O32040	bacillus su
9	21	100.0	69	1	Y010_TROWT	P59486	tropheryma
10	21	100.0	69	1	YAT1_RHOBL	P05443	rhodopseudo
11	21	100.0	90	1	Y040_CORGL	Q8nu99	corynebacte
12	21	100.0	90	1	YFIM_ECOLI	P46126	escherichia
13	21	100.0	95	1	MGBB_HUMAN	O75556	homo sapien
14	21	100.0	96	1	Y87A_HAEIN	O86229	haemophilus
15	21	100.0	110	1	COX4_BACSU	P24013	bacillus su
16	21	100.0	114	1	YE96_METJA	Q58891	methanococc
17	21	100.0	115	1	TKN1_RABIT	P41540	oryctolagus
18	21	100.0	117	1	NU3M_BRALA	O47429	branchiosto
19	21	100.0	129	1	TKN1_HUMAN	P20366	homo sapien
20	21	100.0	130	1	TKN1_BOVIN	P01289	bos taurus
21	21	100.0	130	1	TKN1_MESAU	Q60541	mesocricetu
22	21	100.0	130	1	TKN1_MOUSE	P41539	mus musculu
23	21	100.0	130	1	TKN1_RAT	P06767	rattus norv
24	21	100.0	131	1	LACY_KLEPN	P59832	klebsiella
25	21	100.0	132	1	OTOR_CHICK	Q9i8p6	gallus gall
26	21	100.0	134	1	YQJE_ECOLI	P42618	escherichia
27	21	100.0	136	1	GLB2_CALSO	P14528	calyptogena
28	21	100.0	137	1	RL16_MYCCA	P02415	mycoplasma
29	21	100.0	166	1	YQ24_BACAN	Q9rn08	bacillus an
30	21	100.0	167	1	NU6M_POLOR	Q95919	polypterus
31	21	100.0	185	1	LYG_ANSAN	P00718	anser anser
32	21	100.0	185	1	LYG_CYGAT	P00717	cygnus atra
33	21	100.0	185	1	LYG_STRCA	P00719	struthio ca
34	21	100.0	194	1	LSPA_RICPR	Q9zdc4	rickettsia
35	21	100.0	196	1	DCD_WIGBR	Q8d218	wiggleswort
36	21	100.0	196	1	SPMA_BACSU	P35157	bacillus su
37	21	100.0	200	1	Y933_HELPJ	Q9zkr8	helicobacte
38	21	100.0	200	1	Y933_HELPY	O25587	helicobacte
39	21	100.0	201	1	LSPA_RICCN	Q92i62	rickettsia
40	21	100.0	206	1	DCTM_PARPN	Q56347	paracoccus
41	21	100.0	207	1	COX3_BACSU	P24012	bacillus su
42	21	100.0	210	1	MOB1_SCHPO	O94360	schizosacch
43	21	100.0	210	1	YD07_HAEIN	Q57320	haemophilus
44	21	100.0	211	1	LYG_CHICK	P27042	gallus gall
45	21	100.0	213	1	NQRD_CHLCV	Q823p4	chlamydophi

ALIGNMENTS

RESULT 1
TKN4_PSEGU
ID TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; E60409; E60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 8 FGLM 11

RESULT 2
TKN5_PSEGU
ID TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

```
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Substance P-like peptide II (PG-SPII).
OS   Pseudophryne guentheri (Guenther's toadlet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC   Myobatrachinae; Pseudophryne.
OX   NCBI_TaxID=30349;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=90287814; PubMed=2356157;
RA   Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA   Roberts J.D., Melchiorri P., Erspamer V.;
RT   "Six novel tachykinin- and bombesin-related peptides from the skin of
RT   the Australian frog Pseudophryne guntheri.";
RL   Peptides 11:299-304(1990).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; F60409; F60409.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   InterPro; IPR008215; Tachykinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   SMART; SM00203; TK; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      11     11       AMIDATION.
SQ   SEQUENCE   11 AA;  1293 MW;  3A247C2CC9CB1457 CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          8 FGLM 11


RESULT 3
TKNA_CHICK
ID   TKNA_CHICK     STANDARD;      PRT;    11 AA.
AC   P19850;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Substance P.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Intestine;
RX   MEDLINE=88204263; PubMed=2452461;
RA   Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT   "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL   Regul. Pept. 20:171-180(1988).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; JN0023; JN0023.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT   MOD_RES      11     11       AMIDATION.
SQ   SEQUENCE   11 AA;  1377 MW;  21487FE3C9D6C6C7 CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          8 FGLM 11


RESULT 4
TKNA_HORSE
ID   TKNA_HORSE     STANDARD;      PRT;    11 AA.
AC   P01290;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Substance P.
GN   TAC1 OR NKNA OR TAC2 OR NKA.
OS   Equus caballus (Horse), and
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796, 10141;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=Horse;
RA   Studer R.O., Trzeciak A., Lergier W.;
RT   "Isolation and amino-acid sequence of substance P from horse
RT   intestine.";
RL   Helv. Chim. Acta 56:860-866(1973).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=C.porcellus;
RX   MEDLINE=90044685; PubMed=2478925;
RA   Murphy R.;
RT   "Primary amino acid sequence of guinea-pig substance P.";
RL   Neuropeptides 14:105-110(1989).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; A01558; SPHO.
DR   PIR; A60654; A60654.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   InterPro; IPR008215; Tachykinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   SMART; SM00203; TK; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT   MOD_RES      11     11       AMIDATION.
SQ   SEQUENCE   11 AA;  1349 MW;  3E757FE3C9D6C6C7 CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          8 FGLM 11


RESULT 5
TKNA_ONCMY
ID   TKNA_ONCMY     STANDARD;      PRT;    11 AA.
AC   P28499;
DT   01-DEC-1992 (Rel. 24, Created)
```

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DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Substance P.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=92298992; PubMed=1376687;
RA   Jensen J., Conlon J.M.;
RT   "Substance-P-related and neurokinin-A-related peptides from the brain
RT   of the cod and trout.";
RL   Eur. J. Biochem. 206:659-664(1992).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; S23308; S23308.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   InterPro; IPR008215; Tachykinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   SMART; SM00203; TK; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT   MOD_RES      11     11       AMIDATION (BY SIMILARITY).
SQ   SEQUENCE   11 AA;  1358 MW;  214860DEC9D6D1F7 CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          8 FGLM 11


RESULT 6
TKNA_SCYCA
ID   TKNA_SCYCA     STANDARD;      PRT;    11 AA.
AC   P41333;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Substance P.
OS   Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC   Scyliorhinidae; Scyliorhinus.
OX   NCBI_TaxID=7830;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=93292508; PubMed=7685693;
RA   Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
RT   "Primary structures and biological activities of substance-P-related
RT   peptides from the brain of the dogfish, Scyliorhinus canicula.";
RL   Eur. J. Biochem. 214:469-474(1993).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; S33300; S33300.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT   MOD_RES      11     11       AMIDATION.
SQ   SEQUENCE   11 AA;  1278 MW;  214860DEC9D6D867 CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          8 FGLM 11


RESULT 7
PA2S_HUMAN
ID   PA2S_HUMAN     STANDARD;      PRT;    19 AA.
AC   P24606;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Phospholipase A2, spermatozoa (EC 3.1.1.4) (Phosphatidylcholine
DE   2-acylhydrolase) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Semen;
RX   MEDLINE=92118015; PubMed=1731781;
RA   Langlais J., Chafouleas J.G., Ingraham R., Vigneault N., Roberts K.D.;
RT   "The phospholipase A2 of human spermatozoa; purification and partial
RT   sequence.";
RL   Biochem. Biophys. Res. Commun. 182:208-214(1992).
CC   -!- FUNCTION: Believed to play a key role in the acrosome reaction via
CC       the enzymatic hydrolysis of unsaturated fatty acids linked to
CC       membrane phospholipids overlying the acrosome of mammalian
CC       spermatozoa.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family.
DR   PIR; PS0332; PS0332.
DR   GO; GO:0004623; F:phospholipase A2 activity; NAS.
DR   GO; GO:0007340; P:acrosome reaction; NAS.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   PROSITE; PS00118; PA2_HIS; PARTIAL.
DR   PROSITE; PS00119; PA2_ASP; PARTIAL.
KW   Hydrolase; Lipid degradation.
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  2233 MW;  88CE016056C3BEBB CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          5 FGLM 8


RESULT 8
YRZK_BACSU
ID   YRZK_BACSU     STANDARD;      PRT;    56 AA.
AC   O32040;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hypothetical protein yrzK.
GN   YRZK OR BSU27570.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA   Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA   Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA   Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA   Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA   Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA   Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA   Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA   Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA   Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA   Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA   Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA   Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA   Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA   Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA   Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA   Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA   Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z99118; CAB14716.1; -.
DR   PIR; A69983; A69983.
DR   SubtiList; BG13820; yrzK.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   56 AA;  6325 MW;  DD489749F1C2200D CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 70;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         39 FGLM 42


RESULT 9
Y010_TROWT
ID   Y010_TROWT     STANDARD;      PRT;    69 AA.
AC   P59486;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hypothetical UPF0233 membrane protein TWT010/TW010.
GN   TWT010 OR TW010.
OS   Tropheryma whipplei (strain Twist) (Whipple's bacillus), and
OS   Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Micrococcineae; Cellulomonadaceae; Tropheryma.
OX   NCBI_TaxID=203267, 218496;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Twist / Genotype 2A;
RX   MEDLINE=22784088; PubMed=12902375;
RA   Raoult D., Ogata H., Audic S., Robert C., Suhre K., Drancourt M.,
RA   Claverie J.-M.;
RT   "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a
RT   reduced genome.";
RL   Genome Res. 13:1800-1809(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TW08/27;
RX   MEDLINE=22495039; PubMed=12606174;
RA   Bentley S.D., Maiwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
RA   Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
RA   von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA   Barrell B.G., Parkhill J., Relman D.A.;
RT   "Sequencing and analysis of the genome of the Whipple's disease
RT   bacterium Tropheryma whipplei.";
RL   Lancet 361:637-644(2003).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the UPF0233 family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE016850; AAO44107.1; -.
DR   EMBL; BX251410; CAD66702.1; -.
DR   HAMAP; MF_00631; -; 1.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM     14     34       POTENTIAL.
FT   TRANSMEM     45     65       POTENTIAL.
SQ   SEQUENCE   69 AA;  7723 MW;  3C83E5B3F154DD24 CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         21 FGLM 24


RESULT 10
YAT1_RHOBL
ID   YAT1_RHOBL     STANDARD;      PRT;    69 AA.
AC   P05443;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   01-NOV-1988 (Rel. 09, Last annotation update)
DE   ATP synthase subunits region ORF 1 (Fragment).
OS   Rhodopseudomonas blastica.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC   Rhodobacteraceae; Rhodobacter.
OX   NCBI_TaxID=1075;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85058188; PubMed=6209404;
RA   Tybulewicz V.L.J., Falk G., Walker J.E.;
RT   "Rhodopseudomonas blastica atp operon. Nucleotide sequence and
RT   transcription.";
RL   J. Mol. Biol. 179:185-214(1984).
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; Z00018; CAA77307.1; -.
DR   PIR; S04666; S04666.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   69 AA;  7471 MW;  574EB0B6F8529ED9 CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         18 FGLM 21


RESULT 11
Y040_CORGL
ID   Y040_CORGL     STANDARD;      PRT;    90 AA.
AC   Q8NU99;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hypothetical UPF0233 membrane protein Cgl0040.
GN   CGL0040.
OS   Corynebacterium glutamicum (Brevibacterium flavum).
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX   NCBI_TaxID=1718;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA   Nakagawa S.;
RT   "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the UPF0233 family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ----------------------------------------------------------------------
DR   EMBL; AP005274; BAB97433.1; -.
DR   HAMAP; MF_00631; -; 1.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM     38     58       POTENTIAL.
FT   TRANSMEM     67     87       POTENTIAL.
SQ   SEQUENCE   90 AA;  9950 MW;  F9E9E657A4089E5D CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         76 FGLM 79


RESULT 12
YFIM_ECOLI
ID   YFIM_ECOLI     STANDARD;      PRT;    90 AA.
AC   P46126;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hypothetical protein yfiM.
GN   YFIM OR B2586.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97349980; PubMed=9205837;
RA   Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA   Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA   Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA   Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
RA   Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA   Yamagata S., Horiuchi T.;
RT   "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT   - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT   analysis of its sequence features.";
RL   DNA Res. 4:91-113(1997).
RN   [3]
RP   SEQUENCE OF 1-53 FROM N.A.
RX   MEDLINE=91161632; PubMed=2002065;
RA   Dechavigny A., Heacock P.N., Dowhan W.;
RT   "Sequence and inactivation of the pss gene of Escherichia coli.
RT   Phosphatidylethanolamine may not be essential for cell viability.";
RL   J. Biol. Chem. 266:5323-5332(1991).
RN   [4]
RP   SEQUENCE OF 23-90 FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=90368520; PubMed=2118499;
RA   Seol W., Shatkin A.J.;
RT   "A new gene located between pss and rrnG on the Escherichia coli
RT   chromosome.";
RL   J. Bacteriol. 172:4745-4745(1990).
RN   [5]
RP   IDENTIFICATION.
RX   MEDLINE=96032851; PubMed=7567469;
RA   Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
RA   Danchin A.;
RT   "Detection of new genes in a bacterial genome using Markov models for
RT   three gene classes.";
RL   Nucleic Acids Res. 23:3554-3562(1995).
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AE000345; AAC75639.1; -.
DR   EMBL; D90886; BAA16471.1; -.
DR   EMBL; D90887; BAA16474.1; -.
DR   EMBL; M58699; -; NOT_ANNOTATED_CDS.
DR   EMBL; X75467; -; NOT_ANNOTATED_CDS.
DR   EMBL; X53027; -; NOT_ANNOTATED_CDS.
DR   PIR; A65037; A65037.
DR   EcoGene; EG12857; yfiM.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   90 AA;  9931 MW;  31E717CCECA6CE14 CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 FGLM 4
              ||||
Db         42 FGLM 45


RESULT 13
MGBB_HUMAN
ID   MGBB_HUMAN      STANDARD;      PRT;    95 AA.
AC   O75556;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Mammaglobin B precursor (Mammaglobin 2) (Lipophilin C) (Lacryglobin)
DE   (Secretoglobin family 2A member 1).
GN   SCGB2A1 OR MGB2 OR UGB3 OR LIPHC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99026127; PubMed=9806831;
RA   Becker R.M., Darrow C., Zimonjic D.B., Popescu N.C., Watson M.A.,
RA   Fleming T.P.;
RT   "Identification of mammaglobin B, a novel member of the uteroglobin
RT   gene family.";
RL   Genomics 54:70-78(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99167354; PubMed=10066439;
RA   Zhao C., Nguyen T., Yusifov T., Glasgow B.J., Lehrer R.I.;
RT   "Lipophilins: human peptides homologous to rat prostatein.";
RL   Biochem. Biophys. Res. Commun. 256:147-155(1999).
RN   [3]
RP   SEQUENCE OF 19-85.
RC   TISSUE=Tears;
RX   MEDLINE=98163342; PubMed=9504814;
RA   Molloy M.P., Bolis S., Herbert B.R., Ou K., Tyler M.I., van Dyk D.D.,
RA   Willcox M.D., Gooley A.A., Williams K.L., Morris C.A., Walsh B.J.;
RT   "Establishment of the human reflex tear two-dimensional polyacrylamide
RT   gel electrophoresis reference map: new proteins of potential
RT   diagnostic value.";
RL   Electrophoresis 18:2811-2815(1997).
RN   [4]
RP   SEQUENCE OF 19-46 AND 60-78, AND MASS SPECTROMETRY.
RC   TISSUE=Tears;
RX   MEDLINE=98385871; PubMed=9720917;
RA   Lehrer R.I., Xu G., Abduragimov A., Dinh N.N., Qu X.-D., Martin D.,
RA   Glasgow B.J.;
RT   "Lipophilin, a novel heterodimeric protein of human tears.";
RL   FEBS Lett. 432:163-167(1998).
CC   -!- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND
CC       ESTRAMUSTINE, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.
CC       MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.
CC   -!- SUBUNIT: HETERODIMER OF A LIPOPHILIN A AND A LIPOPHILIN C
CC       (MAMMAGLOBIN B) MONOMER ASSOCIATED HEAD TO HEAD.
CC   -!- TISSUE SPECIFICITY: Expressed in thymus, trachea, kidney, steroid
CC       responsive tissues (prostate, testis, uterus, breast and ovary)
CC       and salivary gland.
CC   -!- MASS SPECTROMETRY: MW=8854.94; METHOD=Electrospray; RANGE=19-95.
CC   -!- SIMILARITY: Belongs to the uteroglobin family. Lipophilin
CC       subfamily.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF071219; AAC79996.1; -.
DR   EMBL; AJ224173; CAA11865.1; -.
DR   Genew; HGNC:7051; SCGB2A1.
DR   MIM; 604398; -.
DR   GO; GO:0005497; F:androgen binding; NAS.
DR   InterPro; IPR003627; Mamgb/prostatn.
DR   InterPro; IPR000329; Uteroglobin_subf.
DR   InterPro; IPR006038; Uteroglobin_supf.
DR   Pfam; PF01099; Uteroglobin; 1.
DR   ProDom; PD029354; Mamgb/prostatn; 1.
DR   PROSITE; PS00403; UTEROGLOBIN_1; FALSE_NEG.
DR   PROSITE; PS00404; UTEROGLOBIN_2; FALSE_NEG.
KW   Signal; Glycoprotein.
FT   SIGNAL       1     18
FT   CHAIN       19     95       MAMMAGLOBIN B.
FT   CARBOHYD    68     68       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   95 AA;  10884 MW;  0719738289F89F8D CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         77 FGLM 80


RESULT 14
Y87A_HAEIN
ID   Y87A_HAEIN      STANDARD;      PRT;    96 AA.
AC   O86229;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hypothetical protein HI0870.1.
GN   HI0870.1.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC   Pasteurellaceae; Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Rd / KW20 / ATCC 51907;
RX   MEDLINE=95350630; PubMed=7542800;
RA   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA   Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA   McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA   Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA   Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA   Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA   Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA   Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA   Venter J.C.;
RT   "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT   Rd.";
RL   Science 269:496-512(1995).
RN   [2]
RP   IDENTIFICATION.
RA   White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D., Peterson J.,
RA   Hickey E., Dodson R., Gwinn M.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U32769; AAC22539.1; -.
DR   TIGR; HI0870.1; -.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM     27     47       POTENTIAL.
FT   TRANSMEM     50     70       POTENTIAL.
```

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SQ   SEQUENCE   96 AA;  11429 MW;  1A0FF09659E11150 CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 96;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         13 FGLM 16


RESULT 15
COX4_BACSU
ID   COX4_BACSU     STANDARD;      PRT;   110 AA.
AC   P24013;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Cytochrome c oxidase polypeptide IVB (EC 1.9.3.1) (Cytochrome aa3
DE   subunit 4B) (Caa-3605 subunit 4B).
GN   CTAF OR BSU14920.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=91146590; PubMed=1847686;
RA   Saraste M., Metso T., Nakari T., Jalli T., Lauraeus M.,
RA   van der Oost J.;
RT   "The Bacillus subtilis cytochrome-c oxidase. Variations on a
RT   conserved protein theme.";
RL   Eur. J. Biochem. 195:517-525(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RA   Bertero M., Presecan E., Glaser P., Richou A., Danchin A.;
RT   "Bacillus subtilis chromosomal region downstream nprE.";
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA   Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA   Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA   Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA   Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA   Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA   Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA   Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA   Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA   Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA   Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA   Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA   Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA   Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA   Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA   Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA   Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA   Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
CC   -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC       c + 2 H(2)O.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS 3
CC       POTENTIAL TRANSMEMBRANE DOMAINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X54140; CAA38079.1; -.
DR   EMBL; Z98682; CAB11345.1; -.
DR   EMBL; Z99111; CAB13365.1; -.
DR   PIR; G69609; G69609.
DR   SubtiList; BG10218; ctaF.
DR   InterPro; IPR005171; COX4_pro.
DR   Pfam; PF03626; COX4_pro; 1.
KW   Oxidoreductase; Transmembrane; Complete proteome.
SQ   SEQUENCE   110 AA;  12620 MW;  1142CF36A63C3AF9 CRC64;

  Query Match             100.0%;  Score 21;  DB 1;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         32 FGLM 35


Search completed: August 25, 2004, 14:06:19
Job time : 24 secs
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blank sheet

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 13:59:47 ; Search time 121 Seconds
(without alignments)
10.430 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	19	10	Q9S8E2	Q9s8e2 spinacia ol
2	21	100.0	41	16	Q7UFM5	Q7ufm5 rhodopirell
3	21	100.0	46	16	Q87RM6	Q87rm6 vibrio para
4	21	100.0	53	5	Q9TYI4	Q9tyi4 caenorhabdi
5	21	100.0	55	5	O17544	O17544 caenorhabdi
6	21	100.0	55	5	O44360	O44360 ceratitis c
7	21	100.0	58	16	Q8EMW4	Q8emw4 oceanobacil
8	21	100.0	63	6	Q9GML1	Q9gml1 macaca fasc
9	21	100.0	63	16	Q82X04	Q82x04 nitrosomona
10	21	100.0	64	5	Q86H30	Q86h30 dictyosteli
11	21	100.0	67	10	Q8GTG4	Q8gtg4 lycopersico
12	21	100.0	67	17	Q8TLY1	Q8tly1 methanosarc
13	21	100.0	68	2	Q05625	Q05625 staphylococ
14	21	100.0	68	2	Q50886	Q50886 myxococcus
15	21	100.0	72	4	Q9Y494	Q9y494 homo sapien
16	21	100.0	72	5	Q9GP92	Q9gp92 caenorhabdi
17	21	100.0	72	16	Q8CSF7	Q8csf7 staphylococ
18	21	100.0	74	4	Q8IWZ7	Q8iwz7 homo sapien
19	21	100.0	76	4	Q86UU6	Q86uu6 homo sapien
20	21	100.0	78	2	Q8VV82	Q8vv82 colwellia m
21	21	100.0	78	16	Q8UKQ3	Q8ukq3 agrobacteri
22	21	100.0	79	2	Q8KZ14	Q8kz14 uncultured
23	21	100.0	79	8	Q8HN49	Q8hn49 brugia mala
24	21	100.0	80	8	O47577	O47577 onchocerca
25	21	100.0	80	16	Q98NI1	Q98ni1 rhizobium l
26	21	100.0	81	16	Q8XN79	Q8xn79 clostridium
27	21	100.0	81	16	Q8D627	Q8d627 vibrio vuln
28	21	100.0	84	12	Q999Z7	Q999z7 carnation m
29	21	100.0	84	16	Q8E405	Q8e405 streptococc
30	21	100.0	85	17	O26173	O26173 methanobact
31	21	100.0	87	4	Q86UU7	Q86uu7 homo sapien
32	21	100.0	88	9	Q8LT78	Q8lt78 vibriophage
33	21	100.0	88	16	Q7UGH0	Q7ugh0 rhodopirell
34	21	100.0	89	2	Q49761	Q49761 mycobacteri
35	21	100.0	90	9	Q8H9X0	Q8h9x0 pseudomonas
36	21	100.0	90	10	Q94JM6	Q94jm6 oryza sativ
37	21	100.0	90	16	Q8X9F4	Q8x9f4 escherichia
38	21	100.0	90	16	Q7UBW7	Q7ubw7 shigella fl
39	21	100.0	93	2	Q9Z9I6	Q9z9i6 escherichia
40	21	100.0	96	4	Q86UU8	Q86uu8 homo sapien
41	21	100.0	97	2	O68974	O68974 synechococc
42	21	100.0	97	11	Q9Z0K2	Q9z0k2 cavia porce
43	21	100.0	99	16	Q9RD07	Q9rd07 streptomyce
44	21	100.0	102	17	Q9YG57	Q9yg57 aeropyrum p
45	21	100.0	104	16	Q92MW6	Q92mw6 rhizobium m

ALIGNMENTS

RESULT 1
Q9S8E2
ID Q9S8E2 PRELIMINARY; PRT; 19 AA.
AC Q9S8E2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 6.1 kDa nuclear-encoded photosystem II reaction center subunit
DE (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=95340559; PubMed=7615565;
RA Irrgang K.D., Shi L.X., Funk C., Schroder W.P.;
RT "A nuclear-encoded subunit of the photosystem II reaction center.";
RL J. Biol. Chem. 270:17588-17593(1995).
SQ SEQUENCE 19 AA; 2067 MW; 547B56337B5719E7 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 FGLM 4
              ||||
Db         15 FGLM 18
```

RESULT 2
Q7UFM5
ID Q7UFM5 PRELIMINARY; PRT; 41 AA.
AC Q7UFM5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.

```
GN   RB8473.
OS   Rhodopirellula baltica.
OC   Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC   Planctomycetaceae; Pirellula.
OX   NCBI_TaxID=117;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1;
RX   MEDLINE=22735913; PubMed=12835416;
RA   Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA   Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA   Schlesner H., Amann R., Reinhardt R.;
RT   "Complete genome sequence of the marine planctomycete Pirellula sp.
RT   strain 1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR   EMBL; BX294147; CAD78657.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   41 AA;  4390 MW;  50080409436EC192 CRC64;

  Query Match             100.0%;  Score 21;  DB 16;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          4 FGLM 7


RESULT 3
Q87RM6
ID   Q87RM6      PRELIMINARY;      PRT;    46 AA.
AC   Q87RM6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Conserved hypothetical protein.
GN   VP0752.
OS   Vibrio parahaemolyticus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=670;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RIMD 2210633 / Serotype O3:K6;
RX   MEDLINE=22508454; PubMed=12620739;
RA   Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA   Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA   Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT   "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT   distinct from that of V. cholerae.";
RL   Lancet 361:743-749(2003).
DR   EMBL; AP005075; BAC59015.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   46 AA;  5225 MW;  6413FC3DF8186097 CRC64;

  Query Match             100.0%;  Score 21;  DB 16;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         25 FGLM 28


RESULT 4
Q9TYI4
ID   Q9TYI4      PRELIMINARY;      PRT;    53 AA.
AC   Q9TYI4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Protein tyrosine kinase (EC 2.7.1.112) (Fragment).
GN   CEHD-17.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Oates A.C., Wilks A.F.;
RT   "How many PTKs to organise a worm?";
RL   The Worm Breeders Gazette 14:87-87(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
RT   "Sampling the Genomic Pool of Protein Tyrosine Kinase Genes using the
RT   Polymerase Chain Reaction with Genomic DNA.";
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ002903; CAA05738.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   ProDom; PD000001; Prot_kinase; 1.
KW   Kinase; Transferase.
FT   NON_TER       1      1
FT   NON_TER      53     53
SQ   SEQUENCE   53 AA;  6207 MW;  2A352DE56CF2BCF6 CRC64;

  Query Match             100.0%;  Score 21;  DB 5;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         14 FGLM 17


RESULT 5
O17544
ID   O17544      PRELIMINARY;      PRT;    55 AA.
AC   O17544;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Protein tyrosine kinase (EC 2.7.1.112) (Fragment).
GN   CEHD-20.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Oates A.C., Wilks A.F.;
RT   "How many PTKs to organise a worm?";
RL   The Worm Breeders Gazette 14:87-87(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
RT   "Sampling the Genomic Pool of Protein Tyrosine Kinase Genes using the
RT   Polymerase Chain Reaction with Genomic DNA.";
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ002904; CAA05739.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Transferase.
FT   NON_TER       1      1
FT   NON_TER      55     55
SQ   SEQUENCE   55 AA;  6491 MW;  5EEEEC59354164E7 CRC64;
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  Query Match             100.0%;  Score 21;  DB 5;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         15 FGLM 18


RESULT 6
O44360
ID   O44360      PRELIMINARY;      PRT;    55 AA.
AC   O44360;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cytochrome P450 monooxygenase (DU154CC) (Fragment).
GN   CYP6A11.
OS   Ceratitis capitata (Mediterranean fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Tephritoidea; Tephritidae; Ceratitis.
OX   NCBI_TaxID=7213;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Danielson P.B., Foster J.L.M., Cooper S.K., Fogleman J.C.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC       OXIDIZED FLAVOPROTEIN + H(2)O.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR   EMBL; AF028002; AAB94119.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005792; C:microsome; IEA.
DR   GO; GO:0004497; F:monooxygenase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR001128; Cytochrome_P450.
KW   Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW   Microsome; Endoplasmic reticulum.
FT   NON_TER       1       1
SQ   SEQUENCE   55 AA;  6332 MW;  D182E26FF3850513 CRC64;

  Query Match             100.0%;  Score 21;  DB 5;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          3 FGLM 6


RESULT 7
Q8EMW4
ID   Q8EMW4      PRELIMINARY;      PRT;    58 AA.
AC   Q8EMW4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical conserved protein.
GN   OB2726.
OS   Oceanobacillus iheyensis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX   NCBI_TaxID=182710;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX   MEDLINE=22220767; PubMed=12235376;
RA   Takami H., Takaki Y., Uchiyama I.;
RT   "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT   Ridge and its unexpected adaptive capabilities to extreme
RT   environments.";
RL   Nucleic Acids Res. 30:3927-3935(2002).
DR   EMBL; AP004602; BAC14682.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   58 AA;  6332 MW;  87EEE8D5B5BA78AB CRC64;

  Query Match             100.0%;  Score 21;  DB 16;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         21 FGLM 24


RESULT 8
Q9GML1
ID   Q9GML1      PRELIMINARY;      PRT;    63 AA.
AC   Q9GML1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RT   "Isolation of full-length cDNA clones from macaque brain cDNA
RT   libraries.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB047938; BAB12349.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   63 AA;  7040 MW;  9D31A5DF462ED22E CRC64;

  Query Match             100.0%;  Score 21;  DB 6;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         34 FGLM 37


RESULT 9
Q82X04
ID   Q82X04      PRELIMINARY;      PRT;    63 AA.
AC   Q82X04;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   NE0496.
OS   Nitrosomonas europaea.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC   Nitrosomonadaceae; Nitrosomonas.
OX   NCBI_TaxID=915;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 19718 / IFO 14298;
RX   MEDLINE=22586410; PubMed=12700255;
RA   Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA   Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA   Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT   "Complete genome sequence of the ammonia-oxidizing bacterium and
RT   obligate chemolithoautotroph Nitrosomonas europaea.";
RL   J. Bacteriol. 185:2759-2773(2003).
DR   EMBL; BX321857; CAD84407.1; -.
```

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KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   63 AA;  7212 MW;  DB098B79A1452DC5 CRC64;

  Query Match             100.0%;  Score 21;  DB 16;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         38 FGLM 41


RESULT 10
Q86H30
ID   Q86H30      PRELIMINARY;      PRT;    64 AA.
AC   Q86H30;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX4;
RX   MEDLINE=22092622; PubMed=12097910;
RA   Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA   Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA   Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT   "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL   Nature 418:79-85(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX4;
RA   Baumgart C.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC115598; AAO53215.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   64 AA;  7451 MW;  B00C0A0DB8DE71D7 CRC64;

  Query Match             100.0%;  Score 21;  DB 5;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         28 FGLM 31


RESULT 11
Q8GTG4
ID   Q8GTG4      PRELIMINARY;      PRT;    67 AA.
AC   Q8GTG4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   WRKY transcription factor IId-2 (Fragment).
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4081;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Money Maker; TISSUE=Leaf;
RA   Cagna G., Boes A., Ulker B., Zhou A., Wanke D., Somssich I.E.;
RT   "Comparison of WRKY group II transcription factors from plants.";
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY157060; AAN71730.1; -.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   InterPro; IPR003657; WRKY.
DR   Pfam; PF03106; WRKY; 1.
DR   PROSITE; PS50811; WRKY; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   67 AA;  7616 MW;  D11A68FA7D715D92 CRC64;

  Query Match             100.0%;  Score 21;  DB 10;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         61 FGLM 64


RESULT 12
Q8TLY1
ID   Q8TLY1      PRELIMINARY;      PRT;    67 AA.
AC   Q8TLY1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Predicted protein.
GN   MA2891.
OS   Methanosarcina acetivorans.
OC   Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC   Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2214;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C2A / ATCC 35395 / DSM 2834;
RX   MEDLINE=21929760; PubMed=11932238;
RA   Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA   FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA   Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA   Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA   Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA   Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA   Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA   Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA   Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA   Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA   Metcalf W.W., Birren B.;
RT   "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT   and physiological diversity.";
RL   Genome Res. 12:532-542(2002).
DR   EMBL; AE010990; AAM06268.1; -.
KW   Complete proteome.
SQ   SEQUENCE   67 AA;  7934 MW;  644065037B1ECA32 CRC64;

  Query Match             100.0%;  Score 21;  DB 17;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          4 FGLM 7


RESULT 13
Q05625
ID   Q05625      PRELIMINARY;      PRT;    68 AA.
AC   Q05625;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   5-enolpyruvylshikimate-3-phosphate synthase.
OS   Staphylococcus aureus.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1280;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=8325-4;
RX   MEDLINE=93381456; PubMed=8371108;
RA   O'Connell C., Pattee P.A., Foster T.J.;
```

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RT   "Sequence and mapping of the aroA gene of Staphylococcus aureus 8325-
RT   4.";
RL   J. Gen. Microbiol. 139:1449-1460(1993).
DR   EMBL; L05004; AAA71898.1; -.
SQ   SEQUENCE   68 AA;  7956 MW;  3B05C55134265B14 CRC64;

  Query Match             100.0%;  Score 21;  DB 2;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         45 FGLM 48


RESULT 14
Q50886
ID   Q50886      PRELIMINARY;      PRT;    68 AA.
AC   Q50886;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Orf2 protein.
GN   ORF2.
OS   Myxococcus xanthus.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC   Cystobacterineae; Myxococcaceae; Myxococcus.
OX   NCBI_TaxID=34;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DK1050;
RX   MEDLINE=96293442; PubMed=8692912;
RA   Nicolas F.J., Cayuela M.L., Martinez-Argudo I.M., Ruiz-Vazquez R.M.,
RA   Murillo F.J.;
RT   "High mobility group I(Y)-like DNA-binding domains on a bacterial
RT   transcription factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:6881-6885(1996).
DR   EMBL; Z56280; CAA91223.1; -.
SQ   SEQUENCE   68 AA;  7214 MW;  1FB0E21FB48BD763 CRC64;

  Query Match             100.0%;  Score 21;  DB 2;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         10 FGLM 13


RESULT 15
Q9Y494
ID   Q9Y494      PRELIMINARY;      PRT;    72 AA.
AC   Q9Y494;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Gamma preprotachykinin (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood, and Brain;
RA   Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
RT   "Identification of a Delta Isoform of preprotachykinin mRNA in Human
RT   Mononuclear Phagocytes and Lymphocytes.";
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF050657; AAC15703.1; -.
DR   GO; GO:0007268; P:synaptic transmission; IEA.
DR   GO; GO:0007217; P:tachykinin signaling pathway; IEA.
DR   InterPro; IPR008216; Protachykinin.
DR   InterPro; IPR008215; Tachykinin.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   Pfam; PF02202; Tachykinin; 2.
DR   ProDom; PD005598; Protachykinin; 1.
DR   SMART; SM00203; TK; 1.
DR   PROSITE; PS00267; TACHYKININ; 2.
FT   NON_TER       1      1
FT   NON_TER      72     72
SQ   SEQUENCE   72 AA;  8274 MW;  2C02B2BA41EAAD16 CRC64;

  Query Match             100.0%;  Score 21;  DB 4;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db         30 FGLM 33


Search completed: August 25, 2004, 14:09:14
Job time : 126 secs
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Blank Sheet

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 13:40:49 ; Search time 123 Seconds
(without alignments)
9.189 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	4	2	AAW41683	Aaw41683 Peptide u
2	21	100.0	4	2	AAY31075	Aay31075 Non-cross
3	21	100.0	4	3	AAB23026	Aab23026 Human/rat
4	21	100.0	4	3	AAY67577	Aay67577 P antagon
5	21	100.0	4	4	AAB91447	Aab91447 Tachykini
6	21	100.0	4	5	ABB10091	Abb10091 Substance
7	21	100.0	4	5	AAU77846	Aau77846 Tachykini
8	21	100.0	5	2	AAR33009	Aar33009 Alpha-sub
9	21	100.0	5	2	AAR33008	Aar33008 Alpha-sub
10	21	100.0	5	2	AAR33007	Aar33007 Alpha-sub
11	21	100.0	5	2	AAR33010	Aar33010 Alpha-sub
12	21	100.0	5	2	AAR54549	Aar54549 Cholecyst
13	21	100.0	5	2	AAR54551	Aar54551 Cholecyst
14	21	100.0	5	2	AAR54550	Aar54550 Cholecyst
15	21	100.0	5	2	AAR54548	Aar54548 Cholecyst
16	21	100.0	5	2	AAW41687	Aaw41687 Tetrapept
17	21	100.0	5	2	AAW99643	Aaw99643 Substance
18	21	100.0	5	2	AAY50325	Aay50325 Neutrophi
19	21	100.0	5	2	AAW92660	Aaw92660 Human tac
20	21	100.0	5	2	AAW92702	Aaw92702 Human tac
21	21	100.0	5	3	AAB23025	Aab23025 Human/rat
22	21	100.0	5	3	AAY67576	Aay67576 P antagon
23	21	100.0	5	4	AAB91428	Aab91428 Tachykini
24	21	100.0	5	4	AAB91389	Aab91389 Tachykini
25	21	100.0	5	5	ABB10090	Abb10090 Substance
26	21	100.0	5	5	ABB10089	Abb10089 Substance
27	21	100.0	5	5	ABB10088	Abb10088 Substance
28	21	100.0	5	5	AAU77845	Aau77845 Tachykini
29	21	100.0	6	1	AAP40519	Aap40519 Sequence
30	21	100.0	6	1	AAP50694	Aap50694 Sequence
31	21	100.0	6	1	AAP50632	Aap50632 Substance
32	21	100.0	6	1	AAP61486	Aap61486 Peptide h
33	21	100.0	6	2	AAR07893	Aar07893 Cylcopept
34	21	100.0	6	2	AAR07899	Aar07899 Cylcopept
35	21	100.0	6	2	AAR21959	Aar21959 Substance
36	21	100.0	6	2	AAR27690	Aar27690 Cyclic ta
37	21	100.0	6	2	AAR27694	Aar27694 Cyclic ta
38	21	100.0	6	2	AAR27691	Aar27691 Cyclic ta
39	21	100.0	6	2	AAW99692	Aaw99692 Substance
40	21	100.0	6	2	AAW99686	Aaw99686 Substance
41	21	100.0	6	2	AAW92706	Aaw92706 Human tac
42	21	100.0	6	2	AAW92659	Aaw92659 Human tac
43	21	100.0	6	3	AAB03356	Aab03356 Neurokini
44	21	100.0	6	3	AAY67575	Aay67575 P antagon
45	21	100.0	6	3	AAY97917	Aay97917 Neurokini

ALIGNMENTS

RESULT 1
AAW41683
ID AAW41683 standard; peptide; 4 AA.
XX
AC AAW41683;
XX
DT 09-JUN-1998 (first entry)
XX
DE Peptide used in ophthalmic drug to treat corneal disorders.
XX
KW Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;
KW keratitis; insulin like growth factor-I; IGF-I; eye drop.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "C-terminal amide"
XX
PN WO9749419-A1.
XX
PD 31-DEC-1997.
XX
PF 11-JUN-1997; 97WO-JP002015.
XX
PR 26-JUN-1996; 96JP-00165612.
XX
PA (SANT) SANTEN PHARM CO LTD.
XX
PI Nishida T, Nakamura M, Nakata K;
XX
DR WPI; 1998-076907/07.
XX
PT Ophthalmic drug composition containing tetra:peptide - is useful as
PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,
PT dry eye, keratitis.
XX
PS Claim 1; Page 15; 19pp; Japanese.
XX
CC The present sequence represents a tetrapeptide which is the active
CC ingredient in an ophthalmic drug composition. It is used, together with
CC insulin like growth factor-I (IGF-I), to treat corneal disorders such as
CC corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The
CC dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and
CC 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of
CC the composition is eye drops
XX
SQ Sequence 4 AA;

```
  Query Match             100.0%;  Score 21;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 2
AAY31075
ID   AAY31075 standard; peptide; 4 AA.
XX
AC   AAY31075;
XX
DT   21-OCT-1999  (first entry)
XX
DE   Non-crosslinked protein particle peptide 124.
XX
KW   Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
KW   albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /note= "C-terminal amide"
XX
PN   US5945033-A.
XX
PD   31-AUG-1999.
XX
PF   12-NOV-1996;   96US-00747137.
XX
PR   15-JAN-1991;   91US-00641720.
PR   13-OCT-1992;   92US-00959560.
PR   01-JUN-1993;   93US-00069831.
PR   14-MAR-1994;   94US-00212546.
XX
PA   (HEMO-) HEMOSPHERE INC.
XX
PI   Yen RCK;
XX
DR   WPI; 1999-508153/42.
XX
PT   Non-crosslinked protein particles for therapeutic and diagnostic use.
XX
PS   Example 22; Col 103-104; 65pp; English.
XX
CC   This invention describes a novel aqueous suspension of monodisperse
CC   particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is
CC   stable against dissolving upon dilution with an alcohol-free aqueous
CC   medium. The method involves (a) forming an aqueous solution containing
CC   albumin and hemoglobin and (b) treating the aqueous solution with an
CC   alcohol to cause the solution to become turbid. The particles are useful
CC   as agents for in vivo administration, either of their own administration
CC   or as a vehicle for other therapeutic or diagnostic agents. The method
CC   permits the formation of albumin and hemoglobin particles in the
CC   nanometer and micrometer size range, in a form closer to their natural
CC   form than the forms of the prior art. The particles therefore constitute
CC   a more closely controlled agent for in vivo administration, with greater
CC   ease of clearance from the body after their period of usefulness.
CC   AAY30952-Y31135 represent peptides used in the method of the invention
XX
SQ   Sequence 4 AA;

  Query Match             100.0%;  Score 21;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 3
AAB23026
ID   AAB23026 standard; peptide; 4 AA.
XX
AC   AAB23026;
XX
DT   16-JAN-2001  (first entry)
XX
DE   Human/rat tachykinin Substance P C-terminal tetrapeptide.
XX
KW   Substance P; tachykinin; human; rat; magnesium binding defect;
KW   sodium sensitive essential hypertension; insulin resistance;
KW   type 2 diabetes; antibody; immunoassay; quantification.
XX
OS   Homo sapiens.
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /note= "C-terminal amide"
XX
PN   WO200054053-A1.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US003707.
XX
PR   10-MAR-1999;   99US-00265690.
XX
PA   (WELL/) WELLS I C.
XX
PI   Wells IC;
XX
DR   WPI; 2000-587457/55.
XX
PT   Detecting magnesium binding defects associated with abnormal
PT   physiological states such as sodium-sensitive essential hypertension and
PT   type 2 insulin-resistant diabetes mellitus, comprises measuring a
PT   specific pentapeptide in blood.
XX
PS   Disclosure; Page 5; 21pp; English.
XX
CC   The inevntion relates to a method for detecting magnesium binding
CC   defects. The method comprises quantitating a tachykinin C-terminal
CC   pentapeptide (e.g., AAB23025) and its degradation products (e.g.,
CC   AAB23026) in blood using an antibody specific for the generalised
CC   mammalian tachykinin C-terminal pentapeptide Phe-(Phe/Val)-Gly-Leu-Met-
CC   NH2 (AAB23028). The method is useful for detecting cellular magnesium
CC   binding defects which are associated with abnormal physiological states
CC   such as sodium-sensitive essential hypertension and type 2 diabetes
CC   mellitus. The present sequence represents the C-terminal 4 amino acids of
CC   the tachykinin Substance P (AAB23027) from human and rat. This is a
CC   degradation product of the Substance P C-terminal pentapeptide (AAB23025)
CC   and may also be assayed according to the method of the invention
XX
SQ   Sequence 4 AA;

  Query Match             100.0%;  Score 21;  DB 3;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 4
AAY67577
ID   AAY67577 standard; peptide; 4 AA.
XX
```

AC AAY67577;
XX
DT 19-MAY-2000 (first entry)
XX
DE P antagonist peptide #5.
XX
KW Pharmaceutical; veterinary; gonadotropin-releasing hormone; GnRH;
KW pore-forming agent; lecithin; stearin; P antagonist.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "C-terminal amide"
XX
PN WO200004897-A1.
XX
PD 03-FEB-2000.
XX
PF 20-JUL-1999; 99WO-AU000585.
XX
PR 20-JUL-1998; 98AU-00004730.
PR 20-JUL-1998; 98AU-00004731.
PR 13-MAY-1999; 99AU-00000324.
XX
PA (PEPT-) PEPTECH LTD.
XX
PI Trigg TE, Walsh JD, Rathjen DA;
XX
DR WPI; 2000-182528/16.
XX
PT Bioimplant formulation for sustained delivery of an active agent over 7
PT days to 2 years, comprises active agent, pore-forming agent and stearin.
XX
PS Claim 20; Page 21; 37pp; English.
XX
CC The invention provides a pharmaceutical and/or veterinary formulation
CC that comprises 2 -30% of active agents which include a gonadotropin-
CC releasing hormone (GnRH) agonist, 0.5 - 20% of a pore-forming agent which
CC is not lecithin, and the remainder stearin. The formulation is useful as
CC a sustained release implant which can deliver the active agent for a
CC period of 7 days to 2 years. Sequences AAY67573-578 represent P
CC antagonist peptides used in the composition
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 1 FGLM 4

RESULT 5
AAB91447
ID AAB91447 standard; peptide; 4 AA.
XX
AC AAB91447;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:623.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 402; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 1 FGLM 4

RESULT 6
ABB10091
ID ABB10091 standard; peptide; 4 AA.
XX
AC ABB10091;
XX
DT 26-JUL-2002 (first entry)
XX
DE Substance P analog used in wound healing treatment#14.
XX
KW Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;
KW surgical incision; burn.
XX
OS Unidentified.
XX
PN WO200213853-A1.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-JP006933.
XX
PR 10-AUG-2000; 2000JP-00242489.
PR 28-NOV-2000; 2000JP-00361388.
XX

PA (SANT) SANTEN PHARM CO LTD.
PA (NISH/) NISHIDA T.
XX
PI Nishida T, Nakata K, Nakamura M;
XX
DR WPI; 2002-269153/31.
XX
PT Skin wound healing promoters or skin epidermal extension promoters
PT containing substance P analogs and insulin-like growth factor-I for
PT treating wounds like tear, abrasion, surgical incision, skin ulcers or
PT burns.
XX
PS Claim 3; Page 11; 20pp; Japanese.
XX
CC The invention relates to skin wound healing promoters, containing
CC substance P analogs or their pharmaceutically-acceptable salts, and
CC insulin-like growth factor-I as the active ingredient. The promoters are
CC for treating wounds like tears, abrasions, surgical incisions, or skin
CC ulcers and burns. The current sequence represents a substance P analog
CC for use in wound healing treatment
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 1 FGLM 4

RESULT 7
AAU77846
ID AAU77846 standard; peptide; 4 AA.
XX
AC AAU77846;
XX
DT 05-JUN-2002 (first entry)
XX
DE Tachykinin N -terminal tetrapeptide.
XX
KW Tachykinin; substance P; hypertension; hypotensive; antidiabetic;
KW gynaecological; salt-insensitive hypertension; magnesium binding;
KW insulin resistance; type 2 diabetes mellitus; pre-eclampsia; eclampsia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 4. .4
FT /note= "C terminal-amide"
XX
PN WO200211714-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US024909.
XX
PR 09-AUG-2000; 2000US-00635266.
XX
PA (MAGN-) MAGNESIUM DIAGNOSTICS INC.
XX
PI Wells IC;
XX
DR WPI; 2002-280663/32.
XX
PT New monopeptides derived from butadienes, ethylenes and propanes are
PT magnesium binding defect antagonists, useful in the treatment of e.g.
PT hypertension, insulin resistance of type 2 diabetes mellitus and
PT eclampsia.
XX
PS Disclosure; Page 2; 38pp; English.
XX
CC This invention relates to novel therapeutic compounds and methods used
CC for treating mammals with disorders such as salt-insensitive
CC hypertension. The monopeptide compounds of the invention are derived from
CC butadienes, ethylenes and propanes. The compounds of the invention are
CC used to correct a defect in magnesium binding within the plasma membranes
CC of somatic cells which results in a decrease in the intracellular
CC concentration of magnesium ions. These compounds may be used in the
CC treatment of a mammal affected with magnesium binding defect, salt-
CC sensitive (particularly hypertension), insulin resistance of type 2
CC diabetes mellitus and pre-eclampsia/eclampsia. The compounds of the
CC invention have an advantage over prior art compounds in that these
CC compounds are biologically stable. The present sequence represents the a
CC tetrapeptide from the C terminal sequence of tachykinin known as
CC substance P, this peptide is sufficient to correct the magnesium binding
CC defect responsible for causing hypertension
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 1 FGLM 4

RESULT 8
AAR33009
ID AAR33009 standard; peptide; 5 AA.
XX
AC AAR33009;
XX
DT 25-MAR-2003 (revised)
DT 02-APR-1993 (first entry)
XX
DE Alpha-substituted short peptide.
XX
KW CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW improved bioavailability.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "alpha-Me-Leu"
FT Modified-site 5
FT /note= "Met-NH2"
XX
PN WO9219254-A1.
XX
PD 12-NOV-1992.
XX
PF 15-APR-1992; 92WO-US003119.
XX
PR 24-APR-1991; 91US-00690755.
PR 20-MAR-1992; 92US-00852086.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Horwell DC, Hughes J, Richardson RS, Howson W;
XX
DR WPI; 1992-398522/48.
XX
PT New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT depression, cancer, asthma, psychosis, arthritis, etc.
XX
PS Claim 3; Page 41; 46pp; English.
XX
CC The peptide is a specifically claimed example of a group of generically
CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC substituent on an alpha-C atom in the chain. Such substitution may modify

CC the bioavailability, stability or absorbability of the peptide and hence
CC may improve the activity of the peptide as a drug. Depending on the
CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC peptide, etc.), the modified peptides are variously useful for treating
CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC addictive drug withdrawal symptoms, hypertension, heart failure,
CC cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC asthma, bladder dysfunction, psychosis and arthritis; and as
CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 21; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 2 FGLM 5

RESULT 9
AAR33008
ID AAR33008 standard; peptide; 5 AA.
XX
AC AAR33008;
XX
DT 25-MAR-2003 (revised)
DT 02-APR-1993 (first entry)
XX
DE Alpha-substituted short peptide.
XX
KW CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW improved bioavailability.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 2
FT /note= "alpha-Me-Phe"
FT Modified-site 5
FT /note= "Met-NH2"
XX
PN WO9219254-A1.
XX
PD 12-NOV-1992.
XX
PF 15-APR-1992; 92WO-US003119.
XX
PR 24-APR-1991; 91US-00690755.
PR 20-MAR-1992; 92US-00852086.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Horwell DC, Hughes J, Richardson RS, Howson W;
XX
DR WPI; 1992-398522/48.
XX
PT New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT depression, cancer, asthma, psychosis, arthritis, etc.
XX
PS Claim 3; Page 41; 46pp; English.
XX
CC The peptide is a specifically claimed example of a group of generically
CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC substituent on an alpha-C atom in the chain. Such substitution may modify
CC the bioavailability, stability or absorbability of the peptide and hence
CC may improve the activity of the peptide as a drug. Depending on the
CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC peptide, etc.), the modified peptides are variously useful for treating
CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC addictive drug withdrawal symptoms, hypertension, heart failure,
CC cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC asthma, bladder dysfunction, psychosis and arthritis; and as
CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 21; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 2 FGLM 5

RESULT 10
AAR33007
ID AAR33007 standard; peptide; 5 AA.
XX
AC AAR33007;
XX
DT 25-MAR-2003 (revised)
DT 02-APR-1993 (first entry)
XX
DE Alpha-substituted short peptide.
XX
KW CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW improved bioavailability.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "alpha-Me-Phe"
FT Modified-site 5
FT /note= "Met-NH2"
XX
PN WO9219254-A1.
XX
PD 12-NOV-1992.
XX
PF 15-APR-1992; 92WO-US003119.
XX
PR 24-APR-1991; 91US-00690755.
PR 20-MAR-1992; 92US-00852086.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Horwell DC, Hughes J, Richardson RS, Howson W;
XX
DR WPI; 1992-398522/48.
XX
PT New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT depression, cancer, asthma, psychosis, arthritis, etc.
XX
PS Claim 3; Page 41; 46pp; English.
XX
CC The peptide is a specifically claimed example of a group of generically
CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC substituent on an alpha-C atom in the chain. Such substitution may modify
CC the bioavailability, stability or absorbability of the peptide and hence
CC may improve the activity of the peptide as a drug. Depending on the
CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC peptide, etc.), the modified peptides are variously useful for treating
CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC addictive drug withdrawal symptoms, hypertension, heart failure,
CC cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC asthma, bladder dysfunction, psychosis and arthritis; and as

```
CC   contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
CC   25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 5 AA;

  Query Match             100.0%;  Score 21;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 11
AAR33010
ID   AAR33010 standard; peptide; 5 AA.
XX
AC   AAR33010;
XX
DT   25-MAR-2003  (revised)
DT   02-APR-1993  (first entry)
XX
DE   Alpha-substituted short peptide.
XX
KW   CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW   improved bioavailability.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   5
FT                   /note= "alpha-Me-Met-NH2"
XX
PN   WO9219254-A1.
XX
PD   12-NOV-1992.
XX
PF   15-APR-1992;    92WO-US003119.
XX
PR   24-APR-1991;    91US-00690755.
PR   20-MAR-1992;    92US-00852086.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Horwell DC,  Hughes J,  Richardson RS,  Howson W;
XX
DR   WPI; 1992-398522/48.
XX
PT   New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT   treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT   depression, cancer, asthma, psychosis, arthritis, etc.
XX
PS   Claim 3; Page 41; 46pp; English.
XX
CC   The peptide is a specifically claimed example of a group of generically
CC   claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC   substituent on an alpha-C atom in the chain. Such substitution may modify
CC   the bioavailability, stability or absorbability of the peptide and hence
CC   may improve the activity of the peptide as a drug. Depending on the
CC   nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC   peptide, etc.), the modified peptides are variously useful for treating
CC   obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC   addictive drug withdrawal symptoms, hypertension, heart failure,
CC   cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC   asthma, bladder dysfunction, psychosis and arthritis; and as
CC   contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
CC   25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 5 AA;

  Query Match             100.0%;  Score 21;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 12
AAR54549
ID   AAR54549 standard; peptide; 5 AA.
XX
AC   AAR54549;
XX
DT   25-MAR-2003  (revised)
DT   14-DEC-1994  (first entry)
XX
DE   Cholecystokinin analogue peptide #42.
XX
KW   Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
KW   gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
KW   heart failure; cognition; memory enhancement; spasticity; depression;
KW   diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   2
FT                   /label= MePhe
FT   Modified-site   5
FT                   /note= "Amidated C-terminal"
XX
PN   WO9409031-A1.
XX
PD   28-APR-1994.
XX
PF   14-OCT-1993;    93WO-US009809.
XX
PR   19-OCT-1992;    92US-00963169.
PR   08-OCT-1993;    93US-00131693.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Horwell DC,  Howson W,  Hugues J,  Richardson RS;
XX
DR   WPI; 1994-151243/18.
XX
PT   New cholecystokinin analogues - useful e.g. in treatment of pain,
PT   obesity, stroke, anxiety, and gastrointestinal ulcers.
XX
PS   Claim 3; Page 66; 73pp; English.
XX
CC   The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues
CC   of cholecystokinin (CCK) which can be used to treat obesity, anxiety,
CC   gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart
CC   failure, cognition, memory enhancement, spasticity, depression, diabetes,
CC   cancers, asthma, bladder dysfunction, psychosis, arthritis and in the
CC   treatment of substance withdrawl. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 5 AA;

  Query Match             100.0%;  Score 21;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 13
```

```
AAR54551
ID   AAR54551 standard; peptide; 5 AA.
XX
AC   AAR54551;
XX
DT   25-MAR-2003  (revised)
DT   14-DEC-1994  (first entry)
XX
DE   Cholecystokinin analogue peptide #44.
XX
KW   Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
KW   gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
KW   heart failure; cognition; memory enhancement; spasticity; depression;
KW   diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   5
FT                   /label= MeMet
FT                   /note= "Amidated C-terminal"
XX
PN   WO9409031-A1.
XX
PD   28-APR-1994.
XX
PF   14-OCT-1993;    93WO-US009809.
XX
PR   19-OCT-1992;    92US-00963169.
PR   08-OCT-1993;    93US-00131693.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Horwell DC,  Howson W,  Hugues J,  Richardson RS;
XX
DR   WPI; 1994-151243/18.
XX
PT   New cholecystokinin analogues - useful e.g. in treatment of pain,
PT   obesity, stroke, anxiety, and gastrointestinal ulcers.
XX
PS   Claim 3; Page 66; 73pp; English.
XX
CC   The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues
CC   of cholecystokinin (CCK) which can be used to treat obesity, anxiety,
CC   gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart
CC   failure, cognition, memory enhancement, spasticity, depression, diabetes,
CC   cancers, asthma, bladder dysfunction, psychosis, arthritis and in the
CC   treatment of substance withdrawl. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 5 AA;

  Query Match             100.0%;  Score 21;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


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AAR54550
ID   AAR54550 standard; peptide; 5 AA.
XX
AC   AAR54550;
XX
DT   25-MAR-2003  (revised)
DT   14-DEC-1994  (first entry)
XX
DE   Cholecystokinin analogue peptide #43.
XX
KW   Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
KW   gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
KW   heart failure; cognition; memory enhancement; spasticity; depression;
KW   diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   3
FT                   /label= MeLeu
FT   Modified-site   5
FT                   /note= "Amidated C-terminal"
XX
PN   WO9409031-A1.
XX
PD   28-APR-1994.
XX
PF   14-OCT-1993;    93WO-US009809.
XX
PR   19-OCT-1992;    92US-00963169.
PR   08-OCT-1993;    93US-00131693.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Horwell DC,  Howson W,  Hugues J,  Richardson RS;
XX
DR   WPI; 1994-151243/18.
XX
PT   New cholecystokinin analogues - useful e.g. in treatment of pain,
PT   obesity, stroke, anxiety, and gastrointestinal ulcers.
XX
PS   Claim 3; Page 66; 73pp; English.
XX
CC   The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues
CC   of cholecystokinin (CCK) which can be used to treat obesity, anxiety,
CC   gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart
CC   failure, cognition, memory enhancement, spasticity, depression, diabetes,
CC   cancers, asthma, bladder dysfunction, psychosis, arthritis and in the
CC   treatment of substance withdrawl. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 5 AA;

  Query Match             100.0%;  Score 21;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 15
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ID   AAR54548 standard; peptide; 5 AA.
XX
AC   AAR54548;
XX
DT   25-MAR-2003  (revised)
DT   14-DEC-1994  (first entry)
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DE   Cholecystokinin analogue peptide #41.
XX
KW   Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
KW   gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
KW   heart failure; cognition; memory enhancement; spasticity; depression;
KW   diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX
OS   Synthetic.
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FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /label= MePhe
FT   Modified-site   5
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FT /note= "Amidated C-terminal"
XX
PN WO9409031-A1.
XX
PD 28-APR-1994.
XX
PF 14-OCT-1993; 93WO-US009809.
XX
PR 19-OCT-1992; 92US-00963169.
PR 08-OCT-1993; 93US-00131693.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Horwell DC, Howson W, Hugues J, Richardson RS;
XX
DR WPI; 1994-151243/18.
XX
PT New cholecystokinin analogues - useful e.g. in treatment of pain,
PT obesity, stroke, anxiety, and gastrointestinal ulcers.
XX
PS Claim 3; Page 66; 73pp; English.
XX
CC The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues
CC of cholecystokinin (CCK) which can be used to treat obesity, anxiety,
CC gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart
CC failure, cognition, memory enhancement, spasticity, depression, diabetes,
CC cancers, asthma, bladder dysfunction, psychosis, arthritis and in the
CC treatment of substance withdrawl. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 21; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4
||||
Db 2 FGLM 5

Search completed: August 25, 2004, 14:05:51
Job time : 126 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 14:07:19 ; Search time 127 Seconds
(without alignments)
9.909 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	4	14	US-10-230-133-3	Sequence 3, Appli
2	21	100.0	4	14	US-10-053-669-2	Sequence 2, Appli
3	21	100.0	4	16	US-10-695-536-3	Sequence 3, Appli
4	21	100.0	5	12	US-10-134-187-3	Sequence 3, Appli
5	21	100.0	5	14	US-10-053-669-1	Sequence 1, Appli
6	21	100.0	5	16	US-10-688-741-3	Sequence 3, Appli
7	21	100.0	5	16	US-10-346-737A-30	Sequence 30, Appl
8	21	100.0	6	14	US-10-168-789A-38	Sequence 38, Appl
9	21	100.0	7	12	US-10-134-187-2	Sequence 2, Appli
10	21	100.0	7	14	US-10-036-542-110	Sequence 110, App
11	21	100.0	7	14	US-10-036-542-111	Sequence 111, App
12	21	100.0	7	14	US-10-168-789A-37	Sequence 37, Appl
13	21	100.0	7	16	US-10-688-741-2	Sequence 2, Appli
14	21	100.0	8	14	US-10-168-789A-36	Sequence 36, Appl
15	21	100.0	9	12	US-10-134-187-1	Sequence 1, Appli
16	21	100.0	9	14	US-10-036-542-112	Sequence 112, App
17	21	100.0	9	14	US-10-168-789A-35	Sequence 35, Appl
18	21	100.0	9	16	US-10-390-472-6	Sequence 6, Appli
19	21	100.0	9	16	US-10-688-741-1	Sequence 1, Appli
20	21	100.0	10	14	US-10-168-789A-34	Sequence 34, Appl
21	21	100.0	11	9	US-09-935-682-64	Sequence 64, Appl
22	21	100.0	11	10	US-09-988-792-1	Sequence 1, Appli
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24	21	100.0	11	10	US-09-988-792-7	Sequence 7, Appli
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26	21	100.0	11	10	US-09-988-792-10	Sequence 10, Appl
27	21	100.0	11	12	US-09-841-091B-26	Sequence 26, Appl
28	21	100.0	11	12	US-10-343-654-27	Sequence 27, Appl
29	21	100.0	11	13	US-10-002-593-4	Sequence 4, Appli
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33	21	100.0	11	14	US-10-114-823B-24	Sequence 24, Appl
34	21	100.0	11	14	US-10-197-954-130	Sequence 130, App
35	21	100.0	11	14	US-10-251-703-25	Sequence 25, Appl
36	21	100.0	11	14	US-10-168-789A-17	Sequence 17, Appl
37	21	100.0	11	14	US-10-423-714-4	Sequence 4, Appli
38	21	100.0	11	15	US-10-289-009-24	Sequence 24, Appl
39	21	100.0	11	15	US-10-289-009-25	Sequence 25, Appl
40	21	100.0	11	15	US-10-289-009-26	Sequence 26, Appl
41	21	100.0	11	16	US-10-167-627-65	Sequence 65, Appl
42	21	100.0	11	16	US-10-695-536-1	Sequence 1, Appli
43	21	100.0	12	9	US-09-922-093-2	Sequence 2, Appli
44	21	100.0	12	9	US-09-922-093-5	Sequence 5, Appli
45	21	100.0	12	9	US-09-922-093-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-230-133-3
; Sequence 3, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; TITLE OF INVENTION: methods for treatment of abnormal physiological states
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-10-230-133-3

Query Match 100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 FGLM 4
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Db          1 FGLM 4
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RESULT 2
US-10-053-669-2
; Sequence 2, Application US/10053669
; Publication No. US20030077658A1

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; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
;  TITLE OF INVENTION:  for Disease Diagnosis
;  FILE REFERENCE: N1427-005
;  CURRENT APPLICATION NUMBER: US/10/053,669
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 09/265,690
;  PRIOR FILING DATE: 1999-03-10
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: AMIDATION
US-10-053-669-2

  Query Match             100.0%;  Score 21;  DB 14;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
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Qy          1 FGLM 4
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Db          1 FGLM 4


RESULT 3
US-10-695-536-3
; Sequence 3, Application US/10695536
; Publication No. US20040110692A1
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert  Clifton
;  TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
;  TITLE OF INVENTION:  and Methods for Treatment of Abnormal Physiological States
;  FILE REFERENCE: 800812-0008
;  CURRENT APPLICATION NUMBER: US/10/695,536
;  CURRENT FILING DATE:  2003-10-28
;  PRIOR APPLICATION NUMBER: US 10/230,133
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US 09/635,266
;  PRIOR FILING DATE: 2000-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: AMIDATION
US-10-695-536-3

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Qy          1 FGLM 4
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Db          1 FGLM 4


RESULT 4
US-10-134-187-3
; Sequence 3, Application US/10134187
; Publication No. US20030202981A1
; GENERAL INFORMATION:
;  APPLICANT: Kream, Richard M.
;  APPLICANT:  Kream, Richard M.
;  APPLICANT:  Kream, Richard M.
;  TITLE OF INVENTION: Chimeric Hybrid Analgesics
;  FILE REFERENCE: Kream
;  CURRENT APPLICATION NUMBER: US/10/134,187
;  CURRENT FILING DATE:  2002-04-26
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: mammalian
US-10-134-187-3

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Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 5
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; Sequence 1, Application US/10053669
; Publication No. US20030077658A1
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
;  TITLE OF INVENTION:  for Disease Diagnosis
;  FILE REFERENCE: N1427-005
;  CURRENT APPLICATION NUMBER: US/10/053,669
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 09/265,690
;  PRIOR FILING DATE: 1999-03-10
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: AMIDATION
US-10-053-669-1

  Query Match             100.0%;  Score 21;  DB 14;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
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Db          2 FGLM 5


RESULT 6
US-10-688-741-3
; Sequence 3, Application US/10688741
; Publication No. US20040106636A1
; GENERAL INFORMATION:
;  APPLICANT: Kream, Richard M.
;  APPLICANT:  Kream, Richard M.
;  APPLICANT:  Kream, Richard M.
;  TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric
;  TITLE OF INVENTION:  Analgesics
;  FILE REFERENCE: Kream
;  CURRENT APPLICATION NUMBER: US/10/688,741
;  CURRENT FILING DATE:  2003-10-17
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 5
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;   TYPE: PRT
;   ORGANISM: mammalian
US-10-688-741-3

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  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 7
US-10-346-737A-30
; Sequence 30, Application US/10346737A
; Publication No. US20040142379A1
; GENERAL INFORMATION:
;  APPLICANT: St. Hilaire, Phaedria
;  TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS
;  FILE REFERENCE: 11225.16US01
;  CURRENT APPLICATION NUMBER: US/10/346,737A
;  CURRENT FILING DATE:  2003-01-16
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Xaa is T(Sa)
US-10-346-737A-30

  Query Match           100.0%;  Score 21;  DB 16;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 8
US-10-168-789A-38
; Sequence 38, Application US/10168789A
; Publication No. US20030148943A1
; GENERAL INFORMATION:
;  APPLICANT: ITOH, Yasuaki
;  APPLICANT:  NISHI, Kazunori
;  APPLICANT:  KITADA, Chieko
;  APPLICANT:  INATOMI, No. US20030148943A1uhiro
;  TITLE OF INVENTION: No. US20030148943A1el Tachykinin-like Polypeptides and Use Thereo
;  FILE REFERENCE: 2680US0P
;  CURRENT APPLICATION NUMBER: US/10/168,789A
;  CURRENT FILING DATE:  2002-06-20
;  PRIOR APPLICATION NUMBER: PCT/JP00/09083
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: JP 11-362638
;  PRIOR FILING DATE: 1999-12-21
;  PRIOR APPLICATION NUMBER: JP 12-066714
;  PRIOR FILING DATE: 1999-03-10
;  NUMBER OF SEQ ID NOS: 64
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;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: peptide
US-10-168-789A-38

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  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
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Db          3 FGLM 6


RESULT 9
US-10-134-187-2
; Sequence 2, Application US/10134187
; Publication No. US20030202981A1
; GENERAL INFORMATION:
;  APPLICANT: Kream, Richard M.
;  APPLICANT:  Kream, Richard M.
;  APPLICANT:  Kream, Richard M.
;  TITLE OF INVENTION: Chimeric Hybrid Analgesics
;  FILE REFERENCE: Kream
;  CURRENT APPLICATION NUMBER: US/10/134,187
;  CURRENT FILING DATE:  2002-04-26
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: mammalian
US-10-134-187-2

  Query Match           100.0%;  Score 21;  DB 12;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
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Db          4 FGLM 7


RESULT 10
US-10-036-542-110
; Sequence 110, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
;  APPLICANT: Birse et al.
;  TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
;  FILE REFERENCE: PA002P1
;  CURRENT APPLICATION NUMBER: US/10/036,542
;  CURRENT FILING DATE:  2002-01-07
;  PRIOR APPLICATION NUMBER: PCT/US00/19666
;  PRIOR FILING DATE: 2000-07-20
;  PRIOR APPLICATION NUMBER: 60/144,972
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: 60/148,681
;  PRIOR FILING DATE: 1999-08-13
;  PRIOR APPLICATION NUMBER: 60/149,173
;  PRIOR FILING DATE: 1999-08-17
;  PRIOR APPLICATION NUMBER: 60/158,004
;  PRIOR FILING DATE: 1999-10-06
;  PRIOR APPLICATION NUMBER: 60/194,689
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-036-542-110

  Query Match           100.0%;  Score 21;  DB 14;  Length 7;
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Qy          1 FGLM 4
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Db          4 FGLM 7


RESULT 11
US-10-036-542-111
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; Publication No. US20030083481A1
; GENERAL INFORMATION:
;  APPLICANT: Birse et al.
;  TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
;  FILE REFERENCE: PA002P1
;  CURRENT APPLICATION NUMBER: US/10/036,542
;  CURRENT FILING DATE:  2002-01-07
;  PRIOR APPLICATION NUMBER: PCT/US00/19666
;  PRIOR FILING DATE: 2000-07-20
;  PRIOR APPLICATION NUMBER: 60/144,972
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: 60/148,681
;  PRIOR FILING DATE: 1999-08-13
;  PRIOR APPLICATION NUMBER: 60/149,173
;  PRIOR FILING DATE: 1999-08-17
;  PRIOR APPLICATION NUMBER: 60/158,004
;  PRIOR FILING DATE: 1999-10-06
;  PRIOR APPLICATION NUMBER: 60/194,689
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-036-542-111

  Query Match             100.0%;  Score 21;  DB 14;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 12
US-10-168-789A-37
; Sequence 37, Application US/10168789A
; Publication No. US20030148943A1
; GENERAL INFORMATION:
;  APPLICANT: ITOH, Yasuaki
;  APPLICANT:  NISHI, Kazunori
;  APPLICANT:  KITADA, Chieko
;  APPLICANT:  INATOMI, No. US20030148943A1uhiro
;  TITLE OF INVENTION: No. US20030148943A1el Tachykinin-like Polypeptides and Use Thereo
;  FILE REFERENCE: 2680US0P
;  CURRENT APPLICATION NUMBER: US/10/168,789A
;  CURRENT FILING DATE:  2002-06-20
;  PRIOR APPLICATION NUMBER: PCT/JP00/09083
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: JP 11-362638
;  PRIOR FILING DATE: 1999-12-21
;  PRIOR APPLICATION NUMBER: JP 12-066714
;  PRIOR FILING DATE: 1999-03-10
;  NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 37
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: peptide
US-10-168-789A-37

  Query Match             100.0%;  Score 21;  DB 14;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          4 FGLM 7


RESULT 13
US-10-688-741-2
; Sequence 2, Application US/10688741
; Publication No. US20040106636A1
; GENERAL INFORMATION:
;  APPLICANT: Kream, Richard M.
;  APPLICANT:  Kream, Richard M.
;  APPLICANT:  Kream, Richard M.
;  TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric H
;  TITLE OF INVENTION:  Analgesics
;  FILE REFERENCE: Kream
;  CURRENT APPLICATION NUMBER: US/10/688,741
;  CURRENT FILING DATE:  2003-10-17
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: mammalian
US-10-688-741-2

  Query Match             100.0%;  Score 21;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          4 FGLM 7


RESULT 14
US-10-168-789A-36
; Sequence 36, Application US/10168789A
; Publication No. US20030148943A1
; GENERAL INFORMATION:
;  APPLICANT: ITOH, Yasuaki
;  APPLICANT:  NISHI, Kazunori
;  APPLICANT:  KITADA, Chieko
;  APPLICANT:  INATOMI, No. US20030148943A1uhiro
;  TITLE OF INVENTION: No. US20030148943A1el Tachykinin-like Polypeptides and Use There
;  FILE REFERENCE: 2680US0P
;  CURRENT APPLICATION NUMBER: US/10/168,789A
;  CURRENT FILING DATE:  2002-06-20
;  PRIOR APPLICATION NUMBER: PCT/JP00/09083
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: JP 11-362638
;  PRIOR FILING DATE: 1999-12-21
;  PRIOR APPLICATION NUMBER: JP 12-066714
;  PRIOR FILING DATE: 1999-03-10
;  NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 36
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: peptide
US-10-168-789A-36

  Query Match             100.0%;  Score 21;  DB 14;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          5 FGLM 8
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RESULT 15
US-10-134-187-1
; Sequence 1, Application US/10134187
; Publication No. US20030202981A1
; GENERAL INFORMATION:
;  APPLICANT: Kream, Richard M.
;  APPLICANT:  Kream, Richard M.
;  APPLICANT:  Kream, Richard M.
;  TITLE OF INVENTION: Chimeric Hybrid Analgesics
;  FILE REFERENCE: Kream
;  CURRENT APPLICATION NUMBER: US/10/134,187
;  CURRENT FILING DATE:  2002-04-26
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: mammalian
US-10-134-187-1

  Query Match           100.0%;  Score 21;  DB 12;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          6 FGLM 9


Search completed: August 25, 2004, 14:20:09
Job time : 128 secs
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blank sheet

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 25, 2004, 14:05:58 ; Search time 32 Seconds
(without alignments)
6.453 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	4	1	US-08-441-591-63	Sequence 63, Appl
2	21	100.0	4	1	US-08-303-362A-63	Sequence 63, Appl
3	21	100.0	4	4	US-09-265-690C-2	Sequence 2, Appli
4	21	100.0	4	4	US-09-635-266-3	Sequence 3, Appli
5	21	100.0	4	4	US-10-230-133-3	Sequence 3, Appli
6	21	100.0	4	5	PCT-US95-05600-80	Sequence 80, Appl
7	21	100.0	5	1	US-07-934-553-2	Sequence 2, Appli
8	21	100.0	5	1	US-08-225-474-2	Sequence 2, Appli
9	21	100.0	5	2	US-08-070-301-6	Sequence 6, Appli
10	21	100.0	5	2	US-07-737-371E-6	Sequence 6, Appli
11	21	100.0	5	2	US-07-737-371E-48	Sequence 48, Appl
12	21	100.0	5	4	US-09-265-690C-1	Sequence 1, Appli
13	21	100.0	6	1	US-07-934-553-3	Sequence 3, Appli
14	21	100.0	6	1	US-08-225-474-3	Sequence 3, Appli
15	21	100.0	6	1	US-08-430-238-15	Sequence 15, Appl
16	21	100.0	6	2	US-07-737-371E-5	Sequence 5, Appli
17	21	100.0	6	3	US-09-317-125-5	Sequence 5, Appli
18	21	100.0	7	1	US-07-712-828B-7	Sequence 7, Appli
19	21	100.0	7	2	US-07-737-371E-8	Sequence 8, Appli
20	21	100.0	8	2	US-07-737-371E-10	Sequence 10, Appl
21	21	100.0	8	2	US-07-737-371E-56	Sequence 56, Appl
22	21	100.0	9	1	US-08-346-849-6	Sequence 6, Appli
23	21	100.0	9	2	US-07-737-371E-60	Sequence 60, Appl
24	21	100.0	9	2	US-08-293-284A-6	Sequence 6, Appli
25	21	100.0	9	4	US-08-898-300-6	Sequence 6, Appli
26	21	100.0	10	1	US-08-088-322-6	Sequence 6, Appli
27	21	100.0	10	1	US-08-437-820-6	Sequence 6, Appli
28	21	100.0	10	2	US-07-737-371E-9	Sequence 9, Appli
29	21	100.0	10	3	US-09-168-548-2	Sequence 2, Appli
30	21	100.0	10	6	5169865-11	Patent No. 5169865
31	21	100.0	11	1	US-07-899-205-1	Sequence 1, Appli
32	21	100.0	11	1	US-07-934-553-1	Sequence 1, Appli
33	21	100.0	11	1	US-08-184-935-12	Sequence 12, Appl
34	21	100.0	11	1	US-08-269-288-2	Sequence 2, Appli
35	21	100.0	11	1	US-08-338-484-1	Sequence 1, Appli
36	21	100.0	11	1	US-08-175-432-1	Sequence 1, Appli
37	21	100.0	11	1	US-08-462-413-2	Sequence 2, Appli
38	21	100.0	11	1	US-08-225-474-1	Sequence 1, Appli
39	21	100.0	11	1	US-08-391-910-2	Sequence 2, Appli
40	21	100.0	11	1	US-08-418-994-2	Sequence 2, Appli
41	21	100.0	11	1	US-08-480-505-3	Sequence 3, Appli
42	21	100.0	11	1	US-08-391-814-2	Sequence 2, Appli
43	21	100.0	11	1	US-08-167-870-1	Sequence 1, Appli
44	21	100.0	11	1	US-08-428-488-15	Sequence 15, Appl
45	21	100.0	11	1	US-08-255-272-6	Sequence 6, Appli

ALIGNMENTS

```
RESULT 1
US-08-441-591-63
; Sequence 63, Application US/08441591
; Patent No. 5637682
;  GENERAL INFORMATION:
;    APPLICANT:  NIEUWLANDT, D., GOLD, L.  AND WECKER, M.
;    TITLE OF INVENTION:  HIGH-AFFINITY
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE LIGANDS
;    TITLE OF INVENTION:  TO THE TACHYKININ
;    TITLE OF INVENTION:  SUBSTANCE P
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MG storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,591
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/303,362
;      FILING DATE:  9-SEPTEMBER-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/931,473
;      FILING DATE:  17-AUGUST-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/117,991
;      FILING DATE:  8-SEPTEMBER 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX21/C
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-441-591-63

  Query Match             100.0%;  Score 21;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 2
US-08-303-362A-63
; Sequence 63, Application US/08303362A
; Patent No. 5648214
;  GENERAL INFORMATION:
;    APPLICANT:  NIEUWLANDT, D., GOLD, L.  AND WECKER, M.
;    TITLE OF INVENTION:  HIGH-AFFINITY
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE LIGANDS
;    TITLE OF INVENTION:  TO THE TACHYKININ
;    TITLE OF INVENTION:  SUBSTANCE P
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MG storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/303,362A
;      FILING DATE:  9-SEPTEMBER-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/931,473
;      FILING DATE:  17-AUGUST-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/117,991
;      FILING DATE:  8-SEPTEMBER 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-303-362A-63

  Query Match             100.0%;  Score 21;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 3
US-09-265-690C-2
; Sequence 2, Application US/09265690C
; Patent No. 6372440
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
;  TITLE OF INVENTION:  for Disease Diagnosis
;  FILE REFERENCE: 1427001
;  CURRENT APPLICATION NUMBER: US/09/265,690C
;  CURRENT FILING DATE:  1999-03-10
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: AMIDATION
US-09-265-690C-2

  Query Match             100.0%;  Score 21;  DB 4;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 4
US-09-635-266-3
; Sequence 3, Application US/09635266
; Patent No. 6455734
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
;  TITLE OF INVENTION:  methods for treatment of abnormal physiological states
;  FILE REFERENCE: N1427-002
;  CURRENT APPLICATION NUMBER: US/09/635,266
;  CURRENT FILING DATE:  2000-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: AMIDATION
US-09-635-266-3

  Query Match             100.0%;  Score 21;  DB 4;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
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```
Db          1 FGLM 4


RESULT 5
US-10-230-133-3
; Sequence 3, Application US/10230133
; Patent No. 6664420
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
;  TITLE OF INVENTION:  methods for treatment of abnormal physiological states
;  FILE REFERENCE: 2892-106
;  CURRENT APPLICATION NUMBER: US/10/230,133
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 09/635,266
;  PRIOR FILING DATE: 2000-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: AMIDATION
US-10-230-133-3

  Query Match             100.0%;  Score 21;  DB 4;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 6
PCT-US95-05600-80
; Sequence 80, Application PC/TUS9505600
;  GENERAL INFORMATION:
;    APPLICANT:  GOLD, LARRY
;    APPLICANT:  NIEUWLANDT, DAN
;    APPLICANT:  WECKER, MATTHEW
;    APPLICANT:  SCHNEIDER, DANIEL J.
;    APPLICANT:  FEIGON, JULI
;    APPLICANT:  ALLEN, PATRICK
;    APPLICANT:  SULLENGER, BRUCE A.
;    APPLICANT:  DOUDNA, JENNIFER, A.
;    TITLE OF INVENTION:  HIGH-AFFINITY LIGANDS OF
;    TITLE OF INVENTION:  INSULIIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
;    TITLE OF INVENTION:  P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
;    NUMBER OF SEQUENCES:  239
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MG
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05600
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/238,863
;      FILING DATE:  06-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/248,632
;      FILING DATE:  24-MAY-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/303,362
;      FILING DATE:  09-SEPTEMBER-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/361,795
;      FILING DATE:  21-DECEMBER-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/117,991
;      FILING DATE:  08-SEPTEMBER-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/931,473
;      FILING DATE:  17-AUGUST-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX17/PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US95-05600-80

  Query Match             100.0%;  Score 21;  DB 5;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 7
US-07-934-553-2
; Sequence 2, Application US/07934553
; Patent No. 5314690
;  GENERAL INFORMATION:
;    APPLICANT:  PATTERSON, R0Y
;    APPLICANT:  HARRIS, KATHLEEN E
;    TITLE OF INVENTION:  METHOD AND COMPOSITION FOR REDUCING IgE
;    TITLE OF INVENTION:  ANTIBODIES TO SPECIFIC ALLERGENS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TILTON, FALLON, LUNGMUS & CHESTNUT
;      STREET:  100 SOUTH WACKER DRIVE
;      CITY:  CHICAGO
;      STATE:  ILLINOIS
;      COUNTRY:  USA
;      ZIP:  60606-4002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/934,553
;      FILING DATE:  19920821
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/705,071
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FENTRESS, SUSAN B
;      REGISTRATION NUMBER:  31,327
;      REFERENCE/DOCKET NUMBER:  NU-9033CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/456-8000
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-07-934-553-2

  Query Match             100.0%;  Score 21;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 8
US-08-225-474-2
; Sequence 2, Application US/08225474
; Patent No. 5560915
;  GENERAL INFORMATION:
;    APPLICANT:  Patterson, Roy
;    APPLICANT:  Harris, Kathleen E.
;    TITLE OF INVENTION:  Method and Composition for Treating
;    TITLE OF INVENTION:  IgE Mediated Allergies
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Tilton, Fallon, Lungmus & Chestnut
;      STREET:  100 S. Wacker Drive, Suite 960
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-4002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/225,474
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/934,553
;      FILING DATE:  21-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/705,071
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tilton, Timothy L.
;      REGISTRATION NUMBER:  16,926
;      REFERENCE/DOCKET NUMBER:  NU 9033-CIP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312)-456-8000
;      TELEFAX:  (312)-456-7776
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-225-474-2

  Query Match             100.0%;  Score 21;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 9
US-08-070-301-6
; Sequence 6, Application US/08070301
; Patent No. 5871995
;  GENERAL INFORMATION:
;    APPLICANT:  IIDA, Toshio
;    APPLICANT:  KAMINUMA, Toshihiko
;    APPLICANT:  FUSE, Yuka
;    APPLICANT:  TAJIMA, Masahiro
;    APPLICANT:  YANAGI, Mitsuo
;    APPLICANT:  OKAMOTO, Hiroshi
;    APPLICANT:  KISHIMOTO, Jiro
;    APPLICANT:  IFUKU, Ohji
;    APPLICANT:  KATO, Ichiro
;    TITLE OF INVENTION:  ENZYME PARTICIPATING IN C-TERMINAL
;    TITLE OF INVENTION:  AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wegner, Cantor, Mueller & Player, P.C.
;      STREET:  1233 20th Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20036-8218
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/070,301
;      FILING DATE:  24-MAY-1991
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-209687
;      FILING DATE:  15-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-181933
;      FILING DATE:  31-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-76331
;      FILING DATE:  26-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-106412
;      FILING DATE:  24-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-205475
;      FILING DATE:  02-AUG-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  P-450-22830
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-040
;      TELEFAX:  (202) 835-0605
;      TELEX:  440706
;  INFORMATION FOR SEQ ID NO:  6:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-070-301-6

  Query Match             100.0%;  Score 21;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          1 FGLM 4


RESULT 10
US-07-737-371E-6
; Sequence 6, Application US/07737371E
; Patent No. 5876948
;  GENERAL INFORMATION:
;    APPLICANT:  Yankner, Bruce A.
;    TITLE OF INVENTION:  SCREENING METHODS TO IDENTIFY
;    TITLE OF INVENTION:  NEUROTOXIN INHIBITORS (AS AMENDED)
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/737,371E
;      FILING DATE:  29-JUL-1991
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/559,172
;      FILING DATE:  27-JUL-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  00108/028002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-737-371E-6

  Query Match             100.0%;  Score 21;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 11
US-07-737-371E-48
; Sequence 48, Application US/07737371E
; Patent No. 5876948
;  GENERAL INFORMATION:
;    APPLICANT:  Yankner, Bruce A.
;    TITLE OF INVENTION:  SCREENING METHODS TO IDENTIFY
;    TITLE OF INVENTION:  NEUROTOXIN INHIBITORS (AS AMENDED)
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/737,371E
;      FILING DATE:  29-JUL-1991
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/559,172
;      FILING DATE:  27-JUL-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  00108/028002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-737-371E-48

  Query Match             100.0%;  Score 21;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 12
US-09-265-690C-1
; Sequence 1, Application US/09265690C
; Patent No. 6372440
; GENERAL INFORMATION:
;  APPLICANT: Wells, Ibert
;  TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
;  TITLE OF INVENTION:  for Disease Diagnosis
;  FILE REFERENCE: 1427001
;  CURRENT APPLICATION NUMBER: US/09/265,690C
;  CURRENT FILING DATE:  1999-03-10
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: AMIDATION
US-09-265-690C-1
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  Query Match             100.0%;  Score 21;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          2 FGLM 5


RESULT 13
US-07-934-553-3
; Sequence 3, Application US/07934553
; Patent No. 5314690
;  GENERAL INFORMATION:
;    APPLICANT:  PATTERSON, R0Y
;    APPLICANT:  HARRIS, KATHLEEN E
;    TITLE OF INVENTION:  METHOD AND COMPOSITION FOR REDUCING IgE
;    TITLE OF INVENTION:  ANTIBODIES TO SPECIFIC ALLERGENS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TILTON, FALLON, LUNGMUS & CHESTNUT
;      STREET:  100 SOUTH WACKER DRIVE
;      CITY:  CHICAGO
;      STATE:  ILLINOIS
;      COUNTRY:  USA
;      ZIP:  60606-4002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/934,553
;      FILING DATE:  19920821
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/705,071
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FENTRESS, SUSAN B
;      REGISTRATION NUMBER:  31,327
;      REFERENCE/DOCKET NUMBER:  NU-9033CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/456-8000
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-07-934-553-3

  Query Match             100.0%;  Score 21;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          3 FGLM 6


RESULT 14
US-08-225-474-3
; Sequence 3, Application US/08225474
; Patent No. 5560915
;  GENERAL INFORMATION:
;    APPLICANT:  Patterson, Roy
;    APPLICANT:  Harris, Kathleen E.
;    TITLE OF INVENTION:  Method and Composition for Treating
;    TITLE OF INVENTION:  IgE Mediated Allergies
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Tilton, Fallon, Lungmus & Chestnut
;      STREET:  100 S. Wacker Drive, Suite 960
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-4002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/225,474
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/934,553
;      FILING DATE:  21-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/705,071
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tilton, Timothy L.
;      REGISTRATION NUMBER:  16,926
;      REFERENCE/DOCKET NUMBER:  NU 9033-CIP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312)-456-8000
;      TELEFAX:  (312)-456-7776
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-225-474-3

  Query Match             100.0%;  Score 21;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          3 FGLM 6


RESULT 15
US-08-430-238-15
; Sequence 15, Application US/08430238
; Patent No. 5693612
;  GENERAL INFORMATION:
;    APPLICANT:  JONCZYK, ALFRED
;    APPLICANT:  HOLZEMANN, GUNTER
;    APPLICANT:  GOODMAN, SIMON
;    APPLICANT:  KESSLER, HORST
;    APPLICANT:  HAUBNER, ROLAND
;    APPLICANT:  WERMUTH, JOCHEN
;    TITLE OF INVENTION:  Cyclopeptides of the Formula I
;    NUMBER OF SEQUENCES:  15
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPA)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,238
;      FILING DATE:  28-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 4415310.4
;      FILING DATE:  30-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lebovitz, Richard M.
```

```
;       REGISTRATION NUMBER:  37,067
;       REFERENCE/DOCKET NUMBER:  MERCK 1692
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 243-6333
;       TELEFAX:  (703) 243-6410
;   INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  circular
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  N-terminal
US-08-430-238-15

  Query Match             100.0%;  Score 21;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGLM 4
              ||||
Db          3 FGLM 6


Search completed: August 25, 2004, 14:16:53
Job time : 34 secs
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